

STIC Search Report Biotech-Chem Library

STIC Database Tracking Number: 94446

TO: Christine Saoud

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Art Unit: 1647 May 30, 2003

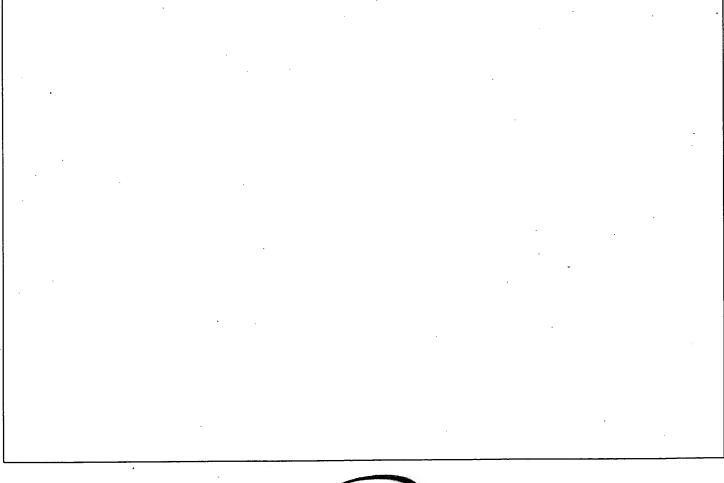


Case Serial Number: 901938

From: P. Sheppard Location: CM1-1E03 Phone: (703) 308-4499

sheppard@uspto.gov

Search Notes





TIC-Biotech/Ch mLib

From: Sent: To:

Subject:

Saoud, Christine Tuesday, May 20, 2003 10:35 AM STIC-Biotech/ChemLib

sequence search

MAY 20 2003

09/901,938

(STIC)

Please search SEQ ID NO:1 and 2 in the patent and commercial databases (no interference, please).

Thank you,

Christine Saoud A.U. 1647 CM1 - 10E03 305-7519 mailbox in 10B19

> Point of Contact P. Sheppard Telephone number: (703) 308-4499

Searcher:	
Phone:	
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TYPE OF SEARCH:
NA Sequences:
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VENDOR/COST (where applic.)
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Human PRO533 cDNA	Human angiogenesis	Human PRO533 cDNA.		PRO533 coding sequ	PRO533	Human PRO533 prote	Human PRO533 cDNA.	 FGF homologue PRO5 	Protein PRO533 cDN	Human polynucleoti	Human fibroblast g	Human fibroblast g	ă	۳	-		Nucleotide sequenc	cDNA encoding mous	Human OST311 polyn	Monkey fibroblast	Human zFGF12 degen	ч	Human fibroblast g	ibroblast	Monkey fibroblast	MK-OST311 DNA sequ	Human OST311 polyn	ST311	Human fibroblast g	polynu	FGF23	otide	otide seguer	sbgFGF-19b	Human PRO9828 nucl

ALIGNMENTS

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RESULT 1
ABK48318
                            Fibroblast growth factor 23; FGF23; hypophosphataemic disorder; autosomal dominant hypophosphataemic rickets, ADHR; fibrous dysplasia; X-linked hypophosphataemic rickets; XLH; tumour induced osteomalacia; TIO; hereditary hypophosphataemic rickets with hypercalciuria; HHRH;
WO200208271-A1
                                                                                                                                                                                                                   hypophosphataemic bone disease; HBD; epidermal nevus syndrome; nephrolithiasis; hyperphosphataemic disorder; mild renal insufficiency; tumoural calcinosis; osteoporosis; dermatomyositis; human; gene; ss.
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The invention describes an isolated polypeptide (I) comprising a C fibroblast growth factor 23 (FGF23) polypeptide or its mutant, variant, C homologue or fragment. (I) is useful for treatment of a hypophosphatemic C disorder such as autosomal dominant hypophosphatemic rickets (ADHR), CC x-linked hypophosphatemic rickets (XIH), hereditary hypophosphatemic C rickets with hypercalciuria (HHRH), hypophosphatemic bone disease (HBD), CC epidermal nevus syndrome, fibrous dysplasia tumour induced osteomalacia CC (TIO), and nephrolithiasis. (I) can also be used in treatment of a CC hyperphosphatemic disorder such as mild renal insufficiency and tumoural CC calcinosis. Osteoporosis, conditions (e.g., dermatcomyositis) involving CC deposition of calcium and phosphate in the arteries or soft tissues of CC described in the invention. Preferably, the nucleic acid or the CC described in the invention. Preferably, the nucleic acid or the CC formation of the invention. Preferably, the nucleic acid or the CC described in the invention. Preferably to treat disease dindividuals. This sequence encodes the novel therapy to treat diseased individuals. This sequence encodes the novel comman fibroblast growth factor 23 (FGF23) studied in the invention.
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Best Local Similarity
Matches 1612; Conserva
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                      The present invention describes DNA encoding a polypeptide having the cativities of inhibiting hypophosphataemia, phosphate transport and calcification, and regulating vitamin D metabolism in vivo. The polypeptide is of human origin (designated OST311) which is localised to chromosome 12p13, or is derived from this by addition, deletion and/or substitution of one or more amino acid residues. OST311 has osteopathic, rephrotropic, antihyperphosphataemic and cytostatic activities. The OST311 polypeptide regulates phosphorus transport and calcium metabolism. OST311 sequences can be used for the treatment and diagnosis of skeletal disorders such as bone cancer, bone formation abnormalities, vitamin D resistance, osteoporosis, Paget's disease and bone calcium deficiency, kidney disorders such as kidney function deficiency, renal phosphate calcales acidosis and Fanconi's disease. The present sequence is used in the exemplification of the present invention.
                                                                                                                                                                                                                                                                                                                                                                                                                                                         11-AUG-2000;
21-SEP-2000;
22-DEC-2000;
19-APR-2001;
                                                                                                                                                                                                                                                                                        Polypeptides useful for regulating phosphate transport and calcium metabolism and DNA encoding them for treatment of phosphate and calcium metabolism disorders, including bone formation abnormalities and kidney
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1021 CCCTTCCACAGGAGGTCCTGTGAGAACCAACCTTTGAGGCCCAAGTCATGGGGTTTCACC 1080 1095 GCCTTCCTCACTCCATATAGAACACCTTTCCCAATAGGAAACCCCAACAGGTAAACTAGA 1154	DR XX PT	P-PSDB;
1081 GCCTTCCTCACTCCATATAGAACACCTTTCCCAATAGGAAACCCCAACAGGTAAACTAGA 1140	rg g t	neurodeg
AATTTCCCCTTCATGAAGGTAGAGAGAGAGGGGTCTCTCCCAACATATTTCTCTTCCTTGT	PS PS	disorder Claim 1;
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1215 GCCTCTCCTCTTTATCACTTTTAAGCATAAAAAAAAAAA	888	factor-2 FGF-20 s
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GCAGTGGGTTCCTGAGCTCAAGACTTTGAAGGTGTAGGGAAGAGGAAATCGGAGATCCCA	ននេះ	and hepat
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1335 GAAGCTTCTCCACTGCCCTATGCATTTATGTTAGATGCCCCGATCCCACTGGCATTTGAG 1394	ያያያ	cancers a
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1395 TGTGCAAACCTTGACATTAACAGCTGAATGGGGCAAGTTGATGAAAACACTACTTTCAAG 1454	\$88 \$	hepatic o
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1501 TGAAAACTTGACAGCTAGACTTGATGCTTGATAATGAGGCAGGAATCATAATAGAAAA 1560	. S	
1575 CTCAGCCTCCCTACAGGGTGAGCACCTTCTGTCTCGCT 1612	δ ? ,	377 AGAG
	ф	337 AGAG
•	δ	437 TTTC
AAC61157 standard; cDNA; 2749 BP.	В	397 TTTC
	Qy	497 CCAG
07-FEB-2001 (first entry)	Дb	457 CCAG
Human fibroblast growth factor-20 (FGF-20) cDNA sequence.	δ	557 TCTG
Fibroblast growth factor-20; FGF-20; cytostatic; nootropic; metastasis; neuroprotective; antiparkinsonian; anticonvulsant; hepatotropic; cancer.	DЬ	517 TCTG
leukaemia; tumour angiogenesis; skeletal dysplasia; Alzheimer; s disease; neurodegenerative disorder; Parkinson's disease; multiple sclerosis;	γQ	617 CCTG
amylotrophic lateral sclerosis; progressive supranuclear palsy; epilepsy; Creutzfeldt-Jakob disease; hepatic disorder; cardiovascular disorder;	DЪ	577 CCTG
haematopoietic disorder; myeloproliferative disorder; human; ss.	Ş	677 CACC
Homo Bapiens.	. B	637 CÁCC
W020060085-A1.	Q ·	737 CCGG
	ДЪ	697 CCGG
27-MAR-2000; 2000WO-US08076.	δ	797 CCCG
02-APR-1999; 99US-0127534. 03-DEC-1999; 99US-0454470.	ф	757 CCCG
(MILL-) MILLENNIUM PHARM INC.	Qy	857 GGGA
Curtis RAJ, Wrighton NC;	o Db	
WPI; 2000-647346/62.	Ş	917 CACC

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P-PSDB; AAY85638.

Novel nucleic acids encoding fibroblast growth factor-20, useful for detecting and modulating FGF-20 and for treating, e.g. cancer, neurodegenerative disorders, hepatic disorders and cardiovascular

Claim 1; Fig 9; 149pp; English.

CC Polynucleotide sequences AAC61155-C61160 encode fibroblast growth CC factor-20 (FGF-20) proteins AAY85637-Y85639. The invention includes CC FGF-20 sequences isolated from humans and monkeys. Proteins, CC polynucleotides, agonists and antagonists of the invention have CC cytostatic; nootropic; neuroprotective; antiparkinsonian; anticonvulsant CC and hepatotropic activity. The peptides, nucleotides and their binding CC agents my be used to modulate the expression or activity of FGF-20, or to CC diagnose aberrant FGF-20 expression. FGF20 activity or expression may be CC down-regulated to treat proliferative or differentiative disorders (e.g. CC cancers and leukaemia), tumour angiogenesis and metastasis, skeletal CC dysplasia, neurodegenerative disorders (e.g. Alzheimer's disease, CC Parkinson's disease, multiple sclerosis, amylotrophic lateral sclerosis, CC progressive supranuclear palsy, epilepsy or Creutzfeldt-Jakob disease), thepatic disorders, cardiovascular disorders and haematopoietic and/or myeloproliferative disorders. ő

Sequence 2749 BP; 747 A; 645 C; 633 G; 724 T; 0 other;

Length

2749;

uery Match 77.9%; Score 1256; DB 21; est Local Similarity 98.1%; Pred. No. 5.5e-293; atches 1271; Conservative 0; Mismatches 25; 917 277 857 757 797 697 737 637 677 577 617 517 557 457 497 397 437 337 377 CACCCTCTTAACCCATCCCTCAGCAAACGCAGCTCTTCCCAAGGACCAGGTCCCTTGAC GGGAACGGGCCCGGAAGGCTGCCCCCTTCGCCAAGTTCATCTAGGGTCGCTGGAAGGG CCGGATGACCCCGGCCCCGGCCTCCTGTTCACAGGAGCTCCCGAGCGCCGAGGGACAACAG CACCCGGAGCGCCGAGGACGACTCGGAGCGGGACCCCCTGAACGTGCTGAAGCCCCGGGC GGATGGCAATGAGTCTTTGCCCTGCCTGTTTTTCTCCATAGGTGCCCTGATGATCAGATC GGGAACGGGCCCGGAAGGCTGCCGCCCCTTCGCCAAGTTCATCTAGGGTCGCTGGAAGGG cererecegadeaaceaearececeraarreaerreaacacececaraceaegegea CCTGTCCCGGAGGAACGAGATCCCCCTAATTCACTTCAACACCCCCCATACCACGGCGGCA ccagacgcriggaaaacgggracgacgrcraccacrcrccrcagrarcacrrccrggrcag CCAGACGCTGGAAAACGGGTACGACGTCTACCACTCTCCTCAGTATCACTTCCTGGTCAG TTTCAGAGGCAACATTTTTGGATCACACTATTTCGACCCGGAGAACTGCAGGTTCCAACA TTTCAGAGGCAACATTTTTGGATCACACTATTTCGACCCGGAGAACTGCAGGTTCCAACA GAATGGCCATGTGGATGGCGCACCCCATCAGACCATCTACAGTGCCCCTGATGATCAGATC 376 CCGGATGACCCCGGCCCCCGCCTCCTGTTCACAGGAGCTCCCGAGCGCCCGAGGACAACAG CACCCGGAGCGCCGAGGACTCGGAGCGGGACCCCTGAACGTGCTGAAGCCCCCGGGC AGAGGATGCTGGCTTTGTGGTGATTACAGGTGTGATGAGCAGAAGATACCTCTGCATGGA AGAGGATGCTGGCTTTGTGGTGATTACAGGTGTGATGAGCAGAAGATACCTCTGCATGGA 436 Indels 0; Gaps 976 916 876 676 816 336 756 696 636 576 616 516 556 456 496 396 0;

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The invention relates to full length GENSET human nucleic acids encoding CC potentially secreted proteins. The nucleic acids and the polypeptides CC they encode may be used in the prevention, treatment and diagnosis of Cd diseases associated with inappropriate GENSET gene expression. For CC example, they be used to treat disorders associated with decreased CG ENSET gene expression by rectifying mutations or deletions in a CC patient's genome that affect the activity of GENSET or by supplementing CC antisense nucleic acid molecules may be administered to down regulate CENSET expression by binding with the cells' own genes and preventing their expression. The sense and antisense nucleic acids may also be used as DNA probes in diagnostic assays to detect and quantitate the CC presence of similar nucleic acid sequences in samples, and hence to GENSET polypeptides may be used as antigens; and hence to CC determine which patients may be in need of restorative therapy. The GENSET polypeptides may be used as antigens in the production of antibodies and in assays to identify modulators (agonists and continued to continue the continued to the continued t
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Full length GENSET human nucleic acids encoding potentially secreted proteins, useful in gene therapy and vaccination against a variety of diseases, and for diagnosis of those diseases -
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Claim
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P-PSDB; AAG89178.
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Sequence 1240 BP; 292 A; 383 C; 325 G; 240 T; 0 other;

Query Match Best Local

Match 76.8%; Local Similarity 99.9%;

Score 1238.4; DE Pred. No. 7e-289;

DB 22;

Length 1240;

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                                                                                                                           Pibroblast growth factor; FGF; zFGF12; chromosome 12; 12q.1.3; neuronal cell; prostatic cell; pancreatic cell; haematopoietic cell; hyperplasia; regeneration; diabetes; amylotrophic lateral sclerosis; stroke; angiogenesis; wound healing; ss.
                                                                                                                                                                                    Nucleotide sequence of fibroblast growth factor homologue zFGF12.
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          mat_peptide
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Chomologue, designated zFGF12. The zFGF12 polypeptides contain a motif
C (see AAB84654) that occurs in all known members of the FGF family, which
is unique to these proteins. This motif is highly conserved in all
C members of the FGF family, however, zFGF12 appears to be unique in that
the conserved Glu is a His (residue 117) substituting a basic amino
c acid (aa) residue for an acidic aa residue. The zFGF12 gene is mapped
to chromosome 12, location 12q.1.3. zFGF12 may be used in the
prevention, diagnosis and treatment of diseases associated with
inappropriate FGF expression: Disorders and processes that may be
prevented, diagnosed, and treated include, for example proliferation
c inappropriate FGF expression: Disorders and processes that may be
grevented, diagnosed, and treated include, for example proliferation
c differentiation of haematopoietic cells, hyperplasia and regeneration,
differentiation flaematopoietic cells, strokes, angiogenesis and
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Matches
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Best Local Similarity
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Claim 16;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              75.1%; Score 1211; DB 22; Length ilarity 100.0%; Pred. No. 2.8e-282; Conservative 0; Mismatches 0; Indels
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                                                                                          Human zFGF12 encoding sequence.
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Location/Qualifiers

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                                                                                                                                                                                                                                                                                                                                                                                       The invention relates to a fibroblast growth factor polypeptide, CC designated zFGF12, comprising a sequence at least 95 % identical to CC residues 25 to 251 of the 251 amino acid sequence, given in the CC specification. The activity of the fibroblast growth factor of the CC invention may be described as vulnerary. zFGF12 can be used to promote CC wound healing of the epidermis, to protect and promote recovery of CC epithelial cells in the gastrointestinal tract, small intestine and oral CC mucosa after chemotherapy or radiation, and to stimulate lung epithelial CC cells after lung injury or complications in neonates following premature CC birth. The polypeptide can also be used to modulate proliferation and CC tinscue. The polypeptide is also useful to stimulate proliferation of cc cultured mesenchymal cells and to identify new family members. The CC current sequence represents the human zFGF12 encoding sequence.
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Best Local Similarity
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          New fibroblast growth factor, designated zFGF12 is for promoting wound healing, protecting and stimulating epithelial cells after chemotherapy or radiation, and stimulating lung epithelial cells after premature
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TACACAGCCACAGCCAGGAACAGCTACCACCTGCAGATCCACAAGAATGGCCATGTGGAT
                                                                                                                                                                                                                                            TCACACCAGCTACTTGCAAGGGAGAAGGAAAAGGCCAGTAAGGCCTGGGCCAGGAGAGTC
                                                             AGAGCCTATCCCAATGCCTCCCCACTGCTCGGCTCCAGCTGGGGTGGCCTGATCCACCTG
                                                                                                           GGGGCCCGCCTCAGGCTCTGGGGTCTGTGCCTTGTGCAGCGTCTGCAGCATGAGCGTCCTC
                                                                                                                                GGGGCCCGCCTCAGGCTCTGGGTCTGTGCCTTGTGCAGCGTCTGCAGCATGAGCGTCCTC
                                                                                                                                                                           CCGACAGGAGTGTCAGGTTTCAATCTCAGCACCAGCCACTCAGAGCAGGGCACGATGTTG
                                                                                                                                                                                                    CCGACAGGAGTGTCAGGTTTCAATCTCAGCACCAGCCACTCAGAGCAGGGCACGATGTTG 152
                                        AGAGCCTATCCCAATGCCTCCCCACTGCTCGGCTCCAGCTGGGGTGGCCTGATCCACCTG
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DB; ABB08352.
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                 TTTTAAGCATA 1243
                                                           TCCCTCAGCAAACGCAGCTCTTCCCAAGGACCAGGTCCCTTGACGTTCCGAGGATGGGAA
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                                             GTAGAGAGAGGGGTCTCCCCAACATATTTCTCTTCCTTGTGCCTCTCCTCTTTATCAC
                                                                                                            AGAACACCTTTCCCGATAGGAAACCCCAACAGGTAAACTAGAAATTTCCCCCTTCATGAAG 1172
                                                                                                                                              TGTGAGAACCAACCTTTGAGGCCCAAGTCATGGGGTTTCACCGCCTTCCTCACTCCATAT
                                                                                                                                                               TGTGAGAACCAACCTTTGAGGCCCAAGTCATGGGGTTTCACCGCCTTCCTCACTCCATAT 1112
                                                                                                                                                                                            AGGTGACAGGGCATGTATGGAATTTGCTGCTTCTCTGGGGTCCCTTCCACAGGAGGTCC
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                                                                                              AGAACACCTTTCCCAATAGGAAACCCCCAACAGGTAAACTAGAAATTTCCCCCTTCATGAAG
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11-AUG-2000; 2000JP-0245144.
21-SEP-2000; 2000JP-0287684.
22-DEC-2000; 2000JP-0391077.
19-APR-2001; 2001JP-0121527.
                                                                                                                                                                                                                                                                                                                                                                                                                                   gene;
                                                                                                                                                                                                                                                                                                                                                                                                                                          bone formation abnormality; vitamin D resistance; Paget's disease; bone calcium deficiency; kidney disorder; kidney function deficiency; renal phosphate leakage; urinary tubule acidosis; Fanconi's disease;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                      OST311; phosphoric acid metabolism; calcium metabolism; calcification; vitamin D metabolism; hypophosphataemia; phosphate transport; cytostatic; chromosome 12p13; osteopathic; nephrotropic; antihyperphosphataemic; phosphorus transport; skeletal disorder; bone cancer; osteoporosis;
                                                                                                                                                                                                                                                                                                                                                    10-AUG-2001;
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                                                                                                                                                                                                                                                                                                                                                                                                              Homo sapiens.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Human OST311 genomic DNA 12p13 SEQ
                                                                                                                                                                                                                                                                                                                                                                                                                                  phosphate leakage;
ds.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          ID
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Polypeptides useful for regulating phosphate transport and calcium metabolism and DNA encoding them for treatment of phosphate and calcium metabolism disorders, including bone formation abnormalities and kidney

2002-227350/28

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Shimada

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Mizutani

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Fukumoto

Claim 20; Page 172-187; 221pp; Japanese

nephrotropic, antihyperphosphataemic and cytostatic activities. The OST311 polypeptide regulates phosphorus transport and calcium metabolism. OST311 sequences can be used for the treatment and diagnosis of skeletal disorders such as bone cancer, bone formation abnormalities, vitamin D resistance, osteoporosis, Paget's disease and bone calcium deficiency; kidney disorders such as kidney function deficiency, renal phosphate leakage, urinary tubule acidosis and Fanconi's disease. The present The present invention describes DNA encoding a polypeptide having the activities of inhibiting hypophosphataemia, phosphate transport and calcification, and regulating vitamin D metabolism in vivo. The polypeptide is of human origin (designated OST311) which is localised to chromosome 12p13, or is derived from this by addition, deletion and/or substitution of one or more amino acid residues. OST311 has osteopathic, sequence is used in the exemplification of the present invention. y the

Sequence 13200 BP; 3710 A; 2982 C; 2903 G; 3605 T; 0 other;

Length 13200;

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                                                                                                                                                                          CACTATTTCGACCCGGAGAACTGCAGGTTCCAACACCAGACGCTGGAAAACGGGTACGAC 10703
                                                                                                                                                                                           CACTATTTCGACCCGGAGAACTGCAGGTTCCAACACCAGACGCTGGAAAACGGGTACGAC 521
CTAATTCACTTCAACACCCCCATACCACGGCGCACACCCGGAGCGCCGAGGACGACTCG
               CTAATTCACTTCAACACCCCCATACCACGGCGCGCACACCCCGGAGCGCCGAGGACTCG
                                                       CTGCCAGGCATGAACCCACCCCGTACTCCCAGTTCCTGTCCCGGAGGAACGAGATCCCC
                                                                         CTGCCAGGCATGAACCCACCCCCGTACTCCCAGTTCCTGTCCCGGAGGAACGAGATCCCC
                                                                                                                 GTCTACCACTCTCAGTATCACTTCCTGGTCAGTCTGGGCCGGGCGAAGAGAGCCCTTC
                                                                                                                                  GTCTACCACTCTCAGTATCACTTCCTGGTCAGTCTGGGCCGGGCGAAGAGAGCCTTC
                                                                                                                                                                                                                                       Conservative
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                                                                                                                                                                                                                                    Score 1151; DB 24;
Pred. No. 2.3e-267;
0; Mismatches 0;
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RESULT 7 ABL50582

ABL50582 standard;

DNA; 13200

19-JUN-2002 ABL50582;

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                                                                           TTGCTGAAATGAGGCAGGAATCATAATAGAAAACTCAGCCTCCCTACAGGGTGAGCACCT
                                                                                                                                 GGAAGAGCTGTCAAAAGACTGGTGGTAGGCTGGTGAAAACTTGACAGCTAGACTTGATGC 1541
                                                                                                                                                                                               ATGGGGCAAGTTGATGAAAACACTACTTTCAAGCCTTCGTTCTTTCCTTGAGCATCTCTGG
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                              TCTGTCTCGCT
                                                                                                                 GGAAGAGCTGTCAAAAGACTGGTGGTAGGCTGGTGAAAACTTGACAGCTAGACTTGATGC
                                                                                                                                                                           ATGGGGCAAGTTGATGAAAACACTACTTTCAAGCCTTCGTTCTTTCCTTGAGCATCTCTGG
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RESULT 8
AAC61159
ID AAC6
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AC AAC6
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AAC61159 standard;

CDNA; 1973

07-FEB-2001 AAC61159

(first entry)

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CCAGACGCTGGAAAAACGGGTACGACGTCTACCACTCTCCTCAGTATCACTTCCTGGTCAG CCAGACGCTGGAAAACGGGTACGACGTCTACCACTCTCCTCAGTATCACTTCCTGGTCAG

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                                                                                                                                                                                                                                                                                              Polymucleotide sequences AAC61155-C61160 encode fibroblast growth CC factor-20 (FGF-20) proteins AAV85637-V85639. The invention includes FGF-20 sequences isolated from humans and monkeys: Proteins, colling of the invention have polymucleotides, agonists of an antagonists of the invention have cytostatic; nootropic; neuroprotective; antiparkinsonian; anticonvulsant and hepatotropic activity. The peptides, nucleotides and their binding cagents my be used to modulate the expression or activity of FGF-20, or to diagnose aberrant FGF-20 expression. FGF20 activity or expression may be down-regulated to treat proliferative or differentiative disorders (e.g. cancers and leukaemia), tumour angiogenesis and metastasis, skeletal dysplasia, neurodegenerative disorders (e.g. Alzheimer's disease, Parkinson's disease, multiple sclerosis, amylotrophic lateral sclerosis, progressive supranuclear palsy, epilepsy or Creutzfeldt-Jakob disease), hepatic disorders, cardiovascular disorders and haematopoietic and/or myeloproliferative disorders.
                                                                                                                                                                                                                   Query Match
Best Local Similarity
Matches 927; Conserv
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                                                                                                                                                                                                                                                                                          Sequence 1973
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Novel nucleic acids encoding fibroblast growth factor-20, useful detecting and modulating FGF-20 and for treating, e.g. cancer, neurodegenerative disorders, hepatic disorders and cardiovascular
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               neuroprotective; antiparkinsonian; anticonvulsant; hepatotropic; cancer; leukaemia; tumour angiogenesis; skeletal dysplasia; Alzheimer's disease; neurodegenerative disorder; Parkinson's disease; multiple sclerosis; amylotrophic lateral sclerosis; progressive supranuclear palsy; epilepsy; Creutzfeldt-Jakob disease; hepatic disorder; cardiovascular disorder; haematopoietic disorder; myeloproliferative disorder; human; ss.
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03-DEC-1999;
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                                                                                         AGAGGATGCTGGCTTTGTGGTGATTACAGGTGTGATGAGCAGAAGATACCTCTGCATGGA
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DB; AAY85639.
TTTCAGAGGCAACATTTTTGGATCACACTATTTCGACCCGGAGAACTGCAGGTTCCAACA
                      TTTCAGAGGCAACATTTTTGGATCACACTATTTCGACCCGGAGAACTGCAGGTTCCAACA
                                                                       AGAGGATGCTGGCTTTGTGGTGATTACAGGTGTGATGAGCAGAAGATACCTCTGCATGGA
                                                                                                                                              GGATGGCAATGAGTCTTTGCCCTGCCTGTTTTTCTCCATAGGTGCCCTGATGATCAGATC
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TTTCCCCTTCATGAAGGTAGAGAAGGGGGTCTCTCCCAACATATTTCTCTTTCCTTGTGC 1216
                                                                                                                   CTTCCTCACTCCATATAGAACACCTTTCCCAATAGGAAACCCCAACAGGTAAACTAGAAA
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                     CTTCCACAGGAGGTCCTGTGAGAACCAACCTTTGAGGCCCAAGTCATGGGGTTTCACCGC
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AAS21376 standard; CDNA; 996

24-OCT-2001 (first entry)

Human cDNA sequence encoding for PRO9828 polypeptide.

RESULT 9
AAS21376
ID AAS2
XX AAS2
XX AAS2
XX Huma
XX Huma
XX Huma
XX Huma
XX Huma
XX Homc
XX H Human secretory and transmembrane; PRO; mammalian; cancer; breast; prostate; cervical; tumour necrosis factor-alpha; TNF-alph cartilage; ear; proliferation; glucose; free fatty acid; skeletal A-peptide; factor VIIA; gene therapy; ss. TNF-alpha; muscle;

07-JUN-2001.

01-DEC-2000; 2000WO-US32678

18-FEB-2000; 2000WO-US07532. 2000WO-US08439. 2000WO-US13705. 99WO-US31243. 2000WO-US00277. 2000WO-US00376. 2000WO-US14042 2000WO-US04914 2000WO-US05004 2000WO-US07377 2000WO-US04414 2000WO-US03565 2000WO-US04341 99WO-US30999 99WO-US30095. 99WO-US28565 99US-0170262

(GETH) GENENTECH INC

Gerritsen \ ME, Goddard A, Go Stewart TA, Tumas Beresini M, Deforge L, Desnoyers L, Filvard A, Godowski PJ, Gurney AL, Shei Tumas D, Watanabe CK, Wood WI, Filvaroff E, L, Sherwood S; Zhang Z; Gao W;

2001-408281/43.

Isolated, secretory and transmembrane PRO polypeptide used to detect other PRO polypeptides, link bioactive molecules to cells expressing PRO polypeptides, and detect the presence of mammalian tumours e.g. lung, breast, prostate, cervical

Claim 3; Fig 265; 813pp; English.

CA AAS21244-AAS21518 encode for novel human secretory and transmembrane CC PRO polypeptides. The PRO polypeptides are useful to detect other CC PRO polypeptides, to link bioactive molecules to cells expressing CC PRO polypeptides, to modulate biological activities of cells expressing CC PRO polypeptides, and to detect the presence of mammalian lung, colon, CC breast, prostate, rectal, cervical or liver tumours by comparing PRO CC polypeptide expression in a cell sample to that in a control sample. CC some of the 275 sequences are also useful to stimulate the release of CC tumour necrosis factor-alpha (TNF-alpha) from human blood, the CC proliferation or differentiation of chondrocytes, the proliferation or colliferation or colliferation or colliferation of inner ear utricular supporting cells or CC gene expression in pericyte cells, the release of proteoglycans from CC cartilage, the proliferation of inner ear utricular supporting cells or CC of T-lymphocytes, the release of a cytckine from peripheral blood CC monocytes (PBMCs), or the proliferation of endothelial cells. Some of CC skeletal muscle cells or by adipocytes, or inhibit binding of A-peptide CC to factor VIIA. The PRO polypeptides can be used in assays to identify CC molecules involved in binding interactions. The polynucleotides encoding CC PRO polypeptides can be used in gene therapy. NA, CC transgenic or knock out animals and can be used in gene therapy.

Sequence 996 BP; 222 A; 320 C; 260 G; 194 T; 0 other;

Query Match Best Local S Matches 798 tch 49.5%; Score 798; DB 22; 1 al Similarity 100.0%; Pred. No. 1.2e-182; 798; Conservative 0; Mismatches 0; Length 996; 0, Gaps

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S 114 AATCTCAGCACCAGCCACTCAGAGCAGGGCACGATGTTGGGGGCCCCGCCTCAGGCTCTGG 173

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AAP44266
ID AAF4
XX AAP4
AC AAF4
AC AAF4
AC BE Huma
CX Huma
CX Huma
CX CCL]
KW CCL]
KW CCL]
KW COS HOmc
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                                                                Human; secreted ar cell death; cancer diagnostic assay;
             WO200073454-A1
                                         Homo sapiens
                                                                                                                        Human PRO9828 nucleotide sequence SEQ ID NO:510.
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                                                                                                                                                                                                             AAF44266 standard;
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eath; cancer; chromosomal mapping; gene mapping; tiss
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AATCTCAGCACCCAGCCCAGAGCAGGGCACGATGTTGGGGGCCCCGCCTCAGGCTCTGG 173 AATCTCAGCACCAGCCACTCAGAGCAGGGCACGATGTTGGGGGGCCCGCCTCAGGCTCTGG

Query Match Best Local (Matches

Local

Similarity

49.5%;
ilarity 100.0%;
Conservative (

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Score 798; DB 22;]
Pred. No. 1.2e-182;
0; Mismatches 0;

Length Indels

996;

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Gaps

0

258 233

798;

Sequence 996

BP; 222 A; 320 C; 260 G; 194 T; 0 other;

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The present invention describes human secreted and transmembrane PRO proteins. The PRO proteins have cytostatic activity. The PRO proteins C can be used for targeted delivery of bioactive molecules, such as C toxins, radiolabels or antibodies, that cause cell death. PRO nucleotide sequences, and their fragments, can be used as hybridisation probes, in C chromosomal and gene mapping, and in the generation of anti-sense RNA CC and DNA. They may also be used to produce transgenic animals which are CC used to develop and screen therapeutically useful reagents. The PRO nucleotide and protein sequence can be used for tissue typing and in CC treating cancer. Anti-PRO antibodies can be used in diagnostic assays. CC ARF44270 to AAF4470 represent PCR primers and hybridisation probes used CC in the isolation of human PRO sequences. AAF44087 to AAF44269 and CC AAB65134 to AAB65300 represent human PRO polynucleotide and protein CC sequences given in the exemplification of the present invention.
                                                                                                                                                                                                                                                                                                                                                                      Roy MA,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  01-DEC-1999;
16-DEC-1999;
20-DEC-1999;
05-JAN-2000;
06-JAN-2000;
11-FEB-2000;
18-FEB-2000;
22-FEB-2000;
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Ferrara N, F
Grimaldi CJ,
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15-SEP-1999;
08-OCT-1999;
30-NOV-1999;
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26-JUL-1999;
28-JUL-1999;
17-AUG-1999;
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23-JUN-1999;
07-JUL-1999;
                                                                                                                                                                                                                                                                       PRO polynucleotides used to produce polypeptides used to target bioactive molecules such as toxins, radiolabels or antibodies, specific cells, to cause targeted cell death -
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P-PSDB; AAB65297.
                                                                                                                                                                                                                                              Claim
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24-FEB-2000;
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N, Fong S, Gerber H, Gerritsen ME, Goddard
i CJ, Gurney AL, Kljavin IJ, Napier MA, Pan
Stewart TA, Tumas D, Watanabe CK, Williams
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99WS-0158663.
99WO-US28313.
99WO-US28301.
99WO-US30095.
99WO-US30095.
99WO-US30091.
2000WO-US00219.
2000WO-US00376.
2000WO-US04341.
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                                                                                                     Human; Alzheimer's disease; amyotrophic lateral sclerosis; ALS; Zollinger-Ellison syndrome; immune system disease; schizophrenia; inflammation; haematopoietic disease; anxiety; feeding disorder; aging; anorexia; depression; cardiovascular disease; sleep disorder; scrure; memory alteration; migraine; stroke; asthma; neuropathy; hypoglycaemia; sexual disorder; growth abnormality; infection; autoimmune disease;
                            anorexia; depression; cardiovascular disease; sleep disorder; seizure; memory alteration; migraine; stroke; asthma; neuropathy; hypoglycaemia; sexual disorder; growth abnormality; infection; autoimmune disease; rheumatoid arthritis; cataractogenesis; angiogenesis; atherosclerosis; cerebral ischaemia; cirrhosis; Huntington's disease; Hodgson's disease; hypercholesterolaemia; headache; amnesia; cardiac arrhythmia; obesity; diabetes mellitus; glomerulonephritis; renovascular hypertension;
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                 sbgFGF-19b gene;
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밁 Ś 밁 S

207 61

GTCCTCAGAGCCTATCCCAATGCCTCCCCACTGCTCGGCTCCAGCTGGGGTGGCCTGATC

266 60 206

GTCCTCAGAGCCTATCCCAATGCCTCCCCACTGCTCGGCTCCAGCTGGGGTGGCCTGATC

ATGTTGGGGGCCCGCCTCAGGCTCTGGGTCTGTGCAGCGTCTGCAGCATGAGC

ATGTTGGGGGCCCGCCTCAGGCTCTGGGGTCTGTGCCAGCGTCTGCAGCATGAGC

Matches

147

Query Match Best Local Similarity

Local C

Conservative

46.9%; Dr 100.0%; Pr 0;

Score 756; DB; Pred. No. 1.5

1.5e-172; DB 22; H, 0 other;

Indels

0;

Gaps

0

Length 756;

Sequence

756 BP; 159

Α, 250

212

G; 135

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CC The invention relates to secreted and membrane associated polypeptides CC and nucleic acid molecules encoding such polypeptides. Sequences of the CC invention are useful for treating diseases such as Alzheimer's disease, CC amyotrophic lateral sclerosis (ALS), Zollinger-Ellison syndrome, disease, CC amyotrophic lateral sclerosis (ALS), Zollinger-Ellison syndrome, diseases CC of the immune system, haematopoietic disease, inflammation, anxiety, CC schizophrenia, feeding disorders, anorexia, depression, social, sexual CC and rewarded behaviour, cardiovascular disease, sleep disorder, learning CC and memory alteration and altered immune response, seizure, migraine, CC cancer, stroke, asthma, neuropathy, aging, sexual disorders, treatment CC of transsexuals, growth abnormalities, obesity, infections, autoimmune CC diseases (e.g. rheumatoid arthritis), cataractogenesis, angiogenesis, CC disorders associated with healthy maintenance of gastric mucosa and crepair of acute and chronic mucosal lesion, lung carcinoma, cerebral CC ischaemia, atherosclerosis, cirrhosis, Huntington's disease, headache, CC ammesia, multiple sclerosis, Hodgson's disease, dilated cardiomyopathy, CC congestive heart failure, cardiac arrhythmias, hypercholesterolaemia, CC viral and onn-viral hepatitis, type I and type II diabetes mellitus, CC glomerulonephritis, renovascular hyperthermia. Polypeptides of the CC invention are used to identify membrane bound and soluble receptors. CC paralyses, tendinitis and malignant hyperthermia. Polypeptides of the CC invention as vaccines for inducing an immunological response ci na mammal. Polynucleotides of the invention are used in gene therapy. CC may are also valuable for chromosome localisation studies and tissue
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          14-FEB-2000;
29-FEB-2000;
18-APR-2000;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        New secreted and membrane associated polypeptides for treating Alzheimer's disease, psoriasis, cancer, enterocolitis, sleep and sexual disorders, stroke, and asthma
                                              expression studies.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        The present sequence is a gene encod a secreted protein of the invention.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Claim 2; Page 53-54; 94pp; English
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; 2000US-0198583.
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/product= "Human sbgFGF-19b protein"
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BEECHAM PLC.
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Nucleotide sequence of human fibroblast growth factor 23 (FGF-23).
                                 29-OCT-2001
                                                                                  AAH75021 standard; DNA; 756
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                                                                                                                                                                                                                     | CCGGCCCCGGCCTCCTGTTCACAGGAGCTCCCGAGCGCCGAGGACAACAGCCCGATGGCC
                                                                                                                                                                                                                                                                                                                              GCCGAGGACCTCGGAGCGGGACCCCCTGAACGTGCTGAAGCCCCCGGGCCCCGGATGACC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            AACATTTTTGGATCACACTATTTCGACCCGGAGAACTGCAGGTTCCAACACCCAGACGCTG
                                                                                                                                                                                                      GCCGAGGACTCGGAGCGGGACCCCCTGAACGTGCTGAAGCCCCGGGGCCCGGATGACC
                                                                                                                                                                                                                                                                                                                                                                                  AGGAACGAGATCCCCCTAATTCACTTCAACACCCCCATACCACGGCGGCACACCCCGGAGC
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RESULT 12
AAH75
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AAH75
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AC AAH75
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DT 29-OC
XX
Pibro
KW Fibro
KW Conge
KW Conge
KW Hintes
KW Giffe
KW Parki
KW Fintes
KW Parki
KW Fintes
KW Parki
KW Fintes
KW Parki
KW Homo
XX
CONGRE
KW Parki
KW Homo
XX
FT CDS
FT CDS
FT XX
WO200
                                                                                                                                                                              Fibroblast growth factor 23; FGF-23; injury; placental cell; ulcer; congenital defect; fertility; abnormal growth; thymus function; leukemia; lymphoma; autoimmune disease; proliferative disorder; differentiation disorder; central nervous system disease; inflammation; parkinson's disease; Alzheimer's disease; Crohn's disease; inflammation; intestinal wound; motility disorder; absorption disorder; stroke; congenital malformation; ischemic vascular disease; myocardial ischemia; peripheral vascular disease; renal artery disease; bone disease; musculoskeletal disease; skeletal myopathy; arthritis; ss.
                                                                                                                                                 sapiens
                                                                                                    Location/Qualifiers
                                   /*tag= a
/product= "fibroblast
                                   growth factor 23
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WO200166596-A2

301

AACATTTTTGGATCACACTATTTCGACCCGGAGAACTGCAGGTTCCAACACCAGACGCTG

360

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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     The present sequence encodes fibroblast growth factor 23 (FGF-23). CC Human FGF-23 polynucleotides and polypeptides are useful for treating a patient suffering from traumatic injury or a condition characterized by dysfunction of or injury to skin cells, a condition characterized by inadequate function of placental cells (e.g. congenital defects, condequate function of placental cells (e.g. congenital defects, condequate function of placental cells (e.g. congenital defects, condequate function of the thymus (e.g. leukemia, lymphoma, autoimmune disease, condition of the thymus, or differentiation disorder of the thymus), or a condition characterized by central nervous system condition characterized by caseful in the treatment of Crohn's disease, healing of intestinal wounds buckers, inflammation, conjuries and surgical anastemoses, motility and absorption disorders, and congenital malformations of the intestine. They are also useful for treating ischemic vascular diseases (e.g. myocardial ischemia/infarction, conjuries and surgical anastemoses, motility and absorption disorders, and congenital malformations of the intestine. They are also useful for conjunction ischemic vascular diseases (e.g. myocardial ischemia/infarction, conjunction or death of skeletal muscle cells, bone cells or supporting cells (e.g. skeletal myopathies, bone disease, or arthritis).
                                                                                                                                                                                                                                                                                                                                                                                                                                                    Matches
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Best Local :
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P-PSDB; AAG63944.
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18-SEP-2000; 2000US-0233368
05-DEC-2000; 2000US-0251649
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Isolated nucleic acids encoding the human and murine fibroblast growth factor 23, useful in the treatment of a condition characterized by inadequate function of placental cells (e.g. congenital defects) and
                447
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                                                                                                                                                                                                                                                                                                61
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AACATTTTTGGATCACACTATTTCGACCCGGAGAACCTGCAGGTTCCAACACCAGACGCTG
                                                                         GGCTTTGTGGTGATTACAGGTGTGATGAGCAGAAGATACCTCTGCATGGATTTCAGAGGC
                                                                                                                                                      GTGGATGGCGCACCCCATCAGACCATCTACAGTGCCCTGATGATCAGATCAGAGGATGCT
                                                  GGCTTTGTGGTGATTACAGGTGTGATGAGCAGAAGATACCTCTGCATGGATTTCAGAGGC
                                                                                                                             GTGGATGGCGCACCCCATCAGACCATCTACAGTGCCCTGATGATCAGATCAGAGGATGCT
                                                                                                                                                                                                                   CACCTGTACACAGC
                                                                                                                                                                                                                                   CACCTGTACACAGCCACAGCCAGGAACAGCTACCACCTGCAGATCCACAAGAATGGCCAT
                                                                                                                                                                                                                                                                                          GTCCTCAGAGCCTATCCCAATGCCTCCCACTGCTCGGCTCCAGCTGGGGTGGCCTGATC
                                                                                                                                                                                                                                                                                                                GTCCTCAGAGCCTATCCCAATGCCTCCCCACTGCTCGGCTCCAGCTGGGGTGGCCTGATC
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                                                                                                                                                                                                               CACAGCCAGGAACAGCTACCACCTGCAGATCCACAAGAATGGCCAT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          46.98;
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; Pred. No. 1.5e-172;
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RESULT 13
AAH75503
AAH75503
ID AAH75
XX X AAH75
AC AAH75
XX 29-OC
XX Pibro
KW Fibro
KW Conge
KW Conge
KW Alzhe
KW Horih

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                                                                                                                                                 08-MAR-2000;
18-SEP-2000;
05-DEC-2000;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Alzheimer's disease; Crohn's disease; intestinal wound; stroke; motility disorder; absorption disorder; intestinal malformation; ischemic vascular disease; myocardial ischemia; myocardial infarction; peripheral vascular disease; renal artery disease; skeletal myopathy; musculoskeletal disease; skeletal muscle cell; bone disease; arthritis;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Fibroblast growth factor 23; FGF-23; injury; placental cell; ulcer; congenital defect; fertility; thymus; leukemia; lymphoma; injury; autoimmune disease; proliferative disorder; differentiation disorder; central nervous system disorder; Parkinson's disease; inflammation;
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                                                                                                                                                                                                                                                   07-MAR-2001; 2001WO-US07468
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/product= "fibroblast growth factor 23 (FGF-23)"
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DR P-PSDB; AAG63947.

XX Isolated nucleic acids encoding the human and murine fibroblast growth pr factor 23, useful in the treatment of a condition characterized by rinadequate function of placental cells (e.g. congenital defects) and the thymus (e.g. leukemia) -

XX Claim 2; Fig 3; 77pp; English.

XX Claim 2; Fig 3; 77pp; English.

XX Crime present sequence encodes fibroblast growth factor 23 (FGF-23).

CC The human FGF-23 polynucleotide and polypeptide are useful for treating comparison of or injury to skin cells, a condition characterized by inadequate function of placental cells (e.g. congenital defects, fettility, or abnormal growth); a condition characterized by inadequate function of placental cells (e.g. congenital defects, fettility, or abnormal growth); a condition characterized by inadequate function of placental cells (e.g. congenital defects, fettility, or abnormal growth); a condition characterized by inadequate function of placental cells (e.g. congenital defects, fettility, or abnormal growth); a condition characterized by central nervous system condition characterized by central nervous system conditions, or a condition characterized by central nervous system conditions, and congenital malformations of the human condition characterized by central nervous system configuration of crohm's disease or Alzheimer's disease. The human configuration disorders, and congenital malformations of the intestine. They are also useful for treating ischemic vascular disease, renal congenital malformations of the intestine. They are also useful for treating ischemic vascular disease, renal congenital malformations of the intestine. They are also useful for treating ischemic vascular disease, renal congenital malformation of skeletal muscle cells, bone cells or supporting cells (e.g. skeletal myopathies, bone disease, con arthritis).

XX Sequence 756 BP; 159 A; 250 C; 212 G; 135 T; 0 other;
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Ś 뮍 Ş 밁 8 밁 밁 S 밁 8 밁 Ş S S 맑 S 밁 Query Match Best Local S Matches 756 421 361 507 301 447 241 387 181 327 121 267 207 147 61 <u>سر</u> GAAAACGGGTACGACGTCTACCACTCTCCTCAGTATCACTTCCTGGTCAGTCTGGGCCGG AGGAACGAGATCCCCCTAATTCACTTCAACACCCCCATACCACGGGGGGACACCCGGAGC GCGAAGAGAGCCTTCCTGCCAGGCATGAACCCCACCCCCGTACTCCCAGTTCCTGTCCCGG GAAAACGGGTACGACGTCTACCACTCTCAGTATCACTTCCTGGTCAGTCTGGGCCGG AACATTTTTGGATCACACTATTTCGACCCGGAGAACTGCAGGTTCCAACACCAGACGCTG GGCTTTGTGGTGATTACAGGTGTGATGAGCAGAAGATACCTCTGCATGGATTTCAGAGGC GTGGATGGCGCACCCCATCAGACCATCTACAGTGCCCTGATGATCAGATCAGAGGATGCT CACCTGTACACAGCCACAGCCAGGAACAGCTACCACCTGCAGATCCACAAGAATGGCCAT GTCCTCAGAGCCTATCCCAATGCCTCCCCACTGCTCGGCTCCAGCTGGGGTGGCCTGATC GTCCTCAGAGCCTATCCCAATGCCTCCCCACTGCTCGGCTCCAGCTGGGGTGGCCTGATC ATGTTGGGGGCCCCCCCCCAGGCTCTGGGTCTGTGCCTTTGTGCAGCGTCTGCAGCATGAGC GCGAAGAGAGCCTTCCTGCCAGGCATGAACCCACCCCGTACTCCCAGTTCCTGTCCCGG AACATTTTTGGATCACACTATTTCGACCCGGAGAACTGCAGGTTCCAACACCAGACGCTG GGCTTTGTGGTGATTACAGGTGTGATGAGCAGAAGATACCTCTGCATGGATTTCAGAGGC GTGGATGGCGCACCCCATCAGACCATCTACAGTGCCCTGATGATCAGATCAGAGGATGCT CACCTGTACACAGCCACAGCCAGGAACAGCTACCACCTGCAGATCCACAAGAATGGCCAT ATGTTGGGGGCCCCGCCTCAGGCTCTGGGGTCTGTGCCTGTGCAGCGTCTGCAGCATGAGC 756; Similarity 46.9%; ilarity 100.0%; Conservative (0; C; 212 G; 135 T; 0 other; Score 756; DB 22; I Pred. No. 1.5e-172; 0; Mismatches 0; 0; Indels Length 756; 0, Gaps 686 480 420 566 506 300 446 240 386 180 326 120 266 60 <u>,</u>

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AGGAACGAGATCCCCCTAATTCACTTCAACACCCCCATACCACGGCGGCACACCCCGGAGC

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                                                                      Query Match
Best Local :
                                                   Matches
                                                                                                                                                                                The invention relates to a DNA (ABN81575) encoding a protein (ABB77581) PGF23 and mutants FGF23 comprising an amino-acid substitution of argining at position 176 to glutamine and/or position 179 to glutamine or tryptophan. The mutants are generated by introducing the following base changes in the nucleic acid sequence: R1760 mutant is generated by G527A; R179Q is generated by G535A; and R179W is generated by C535T. The protein and encoding DNA are applicable in remedies for hyperphosphataemia, including gene therapy.
                                                                                                                                             Sequence 756 BP;
                                                                                                                                                                                                                                                                                                                                                                                                                                                        Human FGF23 applicable i
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29-MAY-2001; 2001JP-0161370.
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llarity 100.0%;
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09-JAN-2001; 2001DE-1000586

DE10100586-C1

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The invention relates to a method for inhibiting expression of a target Gene (ABL91658-ABL91797) in a cell by introducing at least one coligoribonucleotide that has a double-stranded structure consisting of at CC most 49 sequential nucleotide pairs, with at least part of one strand CC complementary with the target gene and has at least one end a CC single-stranded segment of 1-4 nt. The method provides CC cligoribonucleotides for antisense inhibition of gene expression useful CC e.g. for treating tumours but the oligoribonucleotides may also be CC directed against genes present in pathogens (e.g. Plasmodium or CC viruses/viroids, pathogenic on humans, animals or plants) or against CC viruses/viroids, pathogenic on humans, animals or plants) or against CC viruses/viroids, pathogenic on humans. The method provides more CC effective inhibition of gene expression than use of known coligonucleotides, probably because the unpaired overhang increases contained the simple content of 
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Query Match 46.9%; Sc
Best Local Similarity 100.0%; P
Matches 756; Conservative 0;
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... Pred. No. 1.5e-172; Indels
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72	661 AGTGACCCATTAGGGGTGGTCAGGGGCGGTCGAGTGAACACGCACG	661	ф
96	807 AGTGACCCATTAGGGGTGGTCAGGGGGGGGCGGTCGAGGTGAACACGCCTGGGGGAACGGGC 866	807	Ş
99	601 CCGGCCCCGGCCTCCTGTTCACAGGAGCTCCCGAGCGCCGAGGACAACAGCCCGATGGCC 660	601	Db
80	747 CCGGCCCCGGCCTCTTCACAGGAGCTCCCGAGCGCCGAGGACAACAGCCCGATGGCC 806	747	Ş
60	541 GCCGAGGACTCGGAGCGGGACCCCCTGAACGTGCTGAAGCCCCCGGGCCCGGATGACC 600	541	Дb

Search completed: May 29, 2003, 00:01:36 Job time : 445 secs

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Database
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10527.066 Million cell updates/sec
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Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

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49.4 3.1 404 9 AI860694 AI8	49.6 3.1 399 12 BG384192 BG3	49.6 3.1 322 9 AA213024 AA	49.8 3.1 1201 17 CNS016B1 A	50 3.1 1884 12 BF530637 B	50 3.1 468 9 AL514541 · AL	50 3.1 440 9 AI359279 AI	50 3.1 368 9 AA828436 AA	50.2 3.1 544 14 C93698 C	50.2 3.1 153 12 BE874163 B	50.2 3.1 119 12 BG670429 B	50.4 3.1 671 9 AL514097 AL	50.4 3.1 653 12 BG170925 B	50.4 3.1 339 9 AI590021 AI	50.4 3.1 319 9 AA814555 AA	50.4 3.1 316 13 BI506901 B	50.6 3.1 1124 17 CNS073BM A	50.8 3.2 1076 17 CNS015ZO A	27 50.8 3.2 634 9 AL514497 AL5144	51.2 3.2 921 12 BG282532	51.2 3.2 820 12 BE964506	51.4 3.2 1017 17 CNS015K4	51.4 3.2 600 12 BG807855	51.4 3.2 594 10 BB619211	1 51.6 3.2 215 9 AI874303	0 51.8 3.2 839 17 CNS004NB	9 51.8 3.2 530 12 BG308044	8 51.8 3.2 421 9 AI961371	7 51.8 3.2 152 12 BE877210	52 3.2 1024 12 BE965125	5 52.4 3.3 796 17 CNS0118D	4 53.4 3.3 889 17 CNS006MT AI.065	3 53.6 3.3 206 10 AW395897 AW395	2 54 3.3 1201 17 CNS016A0 AL106	1 56.4 3.5 925 17 CNS0091P AL053	0 63.8 4.0 708 12 BG328684 BG328	4.2 950 11 AK007574 AK007	72.6 4.5 888 13 BI919047 BI9	72.6 4.5 835 12 BE889616 BE88
0694 wl15b12.	38419	13024 mw86	0651	530637 602	14541 ĀL51	AI359279 gy27d12.x	oc46c05.s	93698 Dic	6014843	BG670429 DRNBBB03	AL514097	6023236	tr74h11.	of42f07.s	BB170029	AL427304 clone BA0	Drosophi	AL514497 AL514497	BG282532 602406405	BE964506 601658618	AL105550 Drosophil	BG807855 2072-92 M	BB619211 BB619211	AI874303 wm50h10.x	AL054280 Drosophil	BG308044 fm56b06.v	wt17f04 x	60148513	BE965125 601658918	Drogophi.	DASTAS Drosophi	397 sh07h05	AL106482 Drosophil	013 Drosophi	584 60242795	07574 Mus musc	919047 6031808	889616 601512

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REFERENCE AUTHORS RESULT 1 AG095702 VERSION KEYWORDS COMMENT REFERENCE SOURCE ACCESSION DEFINITION TITLE JOURNAL JOURNAL TITLE AUTHORS ORGANISM Submitted (02-AUG-2001) Asao Fujiyama, The Institute of Physical and Chemical Research (RIKEN), Genomic Sciences Center (GSC); 1-7-22 Suehiro-chou, Tsurumi-ku, Yokohama, Kanagawa 230-0045, Japan (B-mail:chimpbes@gsc.riken.go.jp, URL:http://hgp.gsc.riken.go.jp/, Tel:81-45-503-9111, Fax:81-45-503-9170)
Clones are derived from the chimpanzee BAC library PTB This BAC end was generated during the R&D process and may have higher chance of 2 (bases 1 to 719)
Fujiyama, A., Hattori, M., Toyoda, A., 'Totoki, Y., Watanabe, H. and Sakaki, Y. Fujiyama,A., Hattori,M., Toyo Totoki,Y., Watanabe,H. and Sa BAC end sequences of Library Pan troglodytes male lymphoblast BAC Library clone: PTB-096N15.R. AG095702 719
Pan troglodytes DNA, clone:
AG095702 Direct Submission Unpublished Eukaryota; Pan troglodytes Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Pan. AG095702.1 GI:16647544 ., Toyoda,A., Taylor,T.D., Yada,T., and Sakaki,Y. 719 9 bp DNA PTB-096N15.R, DNA, clone_lib:PTB Chimpanzee Male Taylor, T.D., Yada, T., genomic survey sequence linear GSS 03-NOV-2001

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RESULT 2
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                                                                                                                                                                                                                                                    BI789859 470 bp mRNA linear ic44d12.yl Melton Normalized Mixed Mouse Pancreas 1
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                                                                                           466 ATTTCGACCCGGAGAACTGCAAGATTCCAACACCAGACGTTGGAAAACGGGTACGACGTCT
526 ACCACTCTCCTCAGTATCACTTCCTGGTCAGTCTGGGCCGGGCGAAGAGAGCCCTTCCTGC 585
                                                            35
                                                    ACTTCAGCCCAGAGAATTGCAAGTTCCGCCAGTGGACGCTGGAGAATGTCTATGACGTCT
                                                                                                                                                          301;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Library was constructed by Dr. Douglas Melton DNA s
Washington University Genome Sequencing Center For
obtaining a clone please contact: Juliana Brown
(brown@fas.harvard.edu)
MGI:194271 This sequence now available from the IM
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Endocrine Pancreas Consortium
Harvard University, Howard Hughes Medical Institute
Dept of Molecular and Cellular Biology, 7 Divinity Ave, Cambridge,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Lemishka, I., Scearce, M., Brestelli, J., Gradwohl, G., Clifton, S., Hillier, L., Marra, M., Pape, D., Wylie, T., Martin, J., Blistain, A., Schmitt, A., Theising, B., Ritter, E., Ronko, I., Bennett, J., Cardenas, M., Gibbons, M., McCann, R., Cole, R., Tsagareishvili, R., Williams, T., Jackson, Y. and Bowers, Y.
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1 (bases 1 to 470)
Melton,D., Brown,J., Kenty,G.,
Lemishka,I., Scearce,M., Breste
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           for clone orders contact: info@image.llnl.gov
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Email: dmelton@biohp.harvard.edu
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                                                                                                                                                             Conservative
                                                                                                                                                                                                                                                                                      75
                                                                                                                                                                                                                                                                           fractionation. Libraries were amplified once on solid support and plasmid DNA from each library was prepared and mixed in equal amounts. The mixed library DNA was normalized by method #4 from Bonaldo, Lennon, and Soares 1996 Genome Research 6:791-806; 0.5 microgram single-stranded mixed library plasmid DNA was mixed with 5 micrograms PCR product representing mixed library inserts and hybridized to an Ecot of 6. Single-stranded (unhybridized) plasmids were isolated by hydroxyapatite chromatography and used to make this library."

75 a 166 c 139 g 89 t 1 others
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libraries representing EI0.5/12.5 pancreatic bud, E16
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                                                                                                            Email: genome-res@gsc.riken.go.jp,

URL:http://genome.gsc.riken.go.jp/
Carninci,P., Shibata,Y., Hayatsu,N., Sugahara,Y., Shibata,K., Itoh,M., Konno,H., Okazaki,Y., Muramatsu,M. and Hayashizaki,Y.

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Hayatsu, N., Hiramoto, K., Hiraoka, T., Hirozane, T., Imotani, K., Ishii,
Y., Ito, M., Kawai, J., Kojima, Y., Konno, H., Kouda, M., Matsuyama, T.,
Nakamura, M., Nishi, K., Nomura, K., Numasaki, R., Okazaki, Y., Okido, T.,
Saito, R., Sakai, C., Sakai, K., Sakazume, N., Sasaki, D., Sato, K.,
Shibata, K., Shinagawa, A., Shiraki, T., Sogabe, Y., Suzuki, H., Tagawa,
A., Takahashi, F., Takaku-Akahira, S., Tanaka, T., Tomaru, A., Toya, T.,
Watahiki, A., Yasunishi, A., Muramatsu, M. and Hayashizaki, Y.
RIKEN Encyclopedia of Mouse Full-length cDNAs (Akimura, T., et al.
                                                                                                                                                                                                                                                                                                                                                               Laboratory for Genome Exploration Research Group, RIKEN Sciences Center(GSC), Yokohama Institute
The Institute of Physical and Chemical Research (RIKEN)
1-7-22 Suehiro-cho, Tsurumi-ku, Yokohama, Kanagawa 230-Tel: 81-45-503-9222
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     GGAGTGTCAGATATCAAACTCAGAATTAGCCACTCAGTGATGTGCA--ATGCTAGGGACC
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1 (bases Zhao,S.,
                                                         Eukaryota; Metazoa;
Mammalia; Eutheria;
1 (bases 1 to 438)
                                                                                                                                                                                                                         GSS
                                                                                                                                                                                                                                                                                                                                  AQ412342 438 bp DNA RPCI-11-177D20.TJ RPCI-11 Homo sapiens
                                                                                                                                                      Homo sapiens
                                                                                                                                                                                                                                                                            , DNA sequence.
AQ412342
                                                                                                                                                                                                                                                      AQ412342.1
                                                                                                                                                                                         nman.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   e mouse
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    α
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(tissue_type=cerebellum, dev_stage=0 day neonate,

sex=mixed), (tissue_type=hippocampus, dev_stage=adult,

sex=male), (tissue_type=whole body, dev_stage=9 days

embryo, sex=mixed), (tissue_type=lung, dev_stage=13 days

embryo, sex=mixed)"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          tissues
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             note="pooled tissues ; (tissue_type=cerebellum,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    /tissue_type="inner ear"
/dev_stage="adult"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          /db_xref="taxon:10090"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             organism="Mus musculus"
/strain="C57BL/6J"
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       1. .433
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                                                                                         Chordata;
Primates;
                            Nierman, W.,
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Pred. No. 3.6e
0; Mismatches
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                                                                               Craniata; Vertebrata; Euteleostomi; Catarrhini; Hominidae; Homo.
                            Malek,J.,
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                         de Jong, P.
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RESULT 5
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Best Local (
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   TTTCAGAGGCAACATTTTTGGATCACACTATTTC 470
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            AGAGGATGCTGGCTTTGTGGTGATTACAGGTGTGATGAGCAGAAGATACCTCTGCATGGA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          122;
                                                                                                                                                                  Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.

1 (bases 1 to 564)

Mahairas,G.G.; Wallace,J.C., Smith,K., Swartzell,S., Holzman,T.,
                                                                                                                                                                                                                                                                                                                                                  AQ570344 564 bp DNA linear GSS 01-JUN HS_5352_B1_G09_T7A RPCI-11 Human Male BAC Library Homo sapiens genomic_clone Plate=928 Col=17 Row=N, DNA sequence.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Other GSSs: RPCI-11-177D20.TV
Contact: Shaying Zhao, William Nierman,
Department of Eukaryotic Genomics
The Institute for Genomic Research
Contact: Mahairas GG, Wallace JC,
High Throughput Sequencing Center
University of Washington
                                                             99380589
                                                                             scanning the human genome Proc. Natl. Acad. Sci. U.
                                                                                                                                                                                                                                                        Homo sapiens
                                                                                                                                                                                                                                                                                                 AQ570344.1
GSS.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Seq primer: SP6
Class: BAC ends.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             http://www.tigr.org/tdb/humgen/bac_end_search/bac_end_search.html
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 BACPAC Resources (http://bacpac.med.buffalo.edu/ordering)
Research Genet cs (info@resgen.com). BAC end search page:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Clones are derived from the human BAC library RPCI-11. For library availability, please contact Pieter de Jong
                                                                                                             Sequence-tagged connectors: A sequence approach to mapping
                                                                                                                                                                                                                                                                                                                                       AQ570344
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Email: hbe@tigr.org
                                                                                                                                                        Keller,A., Shaker,R.,
                                                                                                                                                                                                                                                                                numan.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        pieter@dejong.med.buffalo.edu). Clones may be purchased from
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          123
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     of BAC End Sequences from Library RPCI-11 for Sequence-Ready
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      /cell_type="Lymphocytes"
/note="Vector: pBACe3.6; Site_1:
RPCII1 Human Male BAC Library"
1 73 c 116 g 126 t
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        /db_xref="GDB:7567675"
/db_xref="taxon:9606"
/clone="RPCI-11-177D20"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      'sex="Male"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        clone_lib="RPCI-11"
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                                                                         Sci. U.S.A. 96 (17), 9739-9744 (1999)
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                                                                                                                                                    Furlong, J.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Score 102.8; DB 17;
Pred. No. 3.4e-08;
0; Mismatches 32;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                366
                                                                                                                                                      Young, J.,
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                                                                                                                                                      Zhao,S.,
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                                                                                                                                                    Adams, M.D.
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                                                                                                                                                                                                   Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.

1 (bases 1 to 741)

NIH-WGC http://mgc.nci.nih.gov/

National Institutes of Health, Mammalian Gene Collection (MGC)

Unpublished (1999)
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          401 Queen Anne Avenue North, Seattle, WA 98109, USA Tel: (206) 616-3618
Fax: (206) 616-3887
Email: jwallace@u washington.edu
Clones are derived from the human BAC library RPCI-11.
found through the I.M.A.G.E. Consortium/LLNL at: http://image.llnl.gov Plate: LLAM9566 row: k column: 08
                                                                                                                                            Email: cgapbs-r@mail.nih.gov
Tissue Procurement: ATCC
                                                                                                                                                                                                                                                                                                                                 Homo sapiens
                                                                                                                                                                                                                                                                                                                                                    human.
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Location/Qualifiers
                                                                                                                                                                                                                                                                                                                                                                                                                  BE869144
                                                                                                                                                                                                                                                                                                                                                                                                                                mRNA sequence
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                                                         CDNA Library Preparation: Life Technologies, Inc.
CDNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL)
DNA Sequencing by: Incyte Genomics, Inc.
Clone distribution: MGC clone distribution information can be
                                                                                                                                                                                  Contact: Robert Strausberg,
                                                                                                                                                                                                                                                                                                                                                                                              BE869144.1
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Male blood DNA was isolated from one randomly chosen deand partially digested with a combination of EcoRI and EcoRI Methylase. Size selected DNA was cloned into the pBACe3.6 vector at EcoRI sites"

1 100 c 138 g 169 t 5 others
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                /note="Vector: pBACe3.6; Site_1: EcoRI; Site_2: EcoRI
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     /db_xref="taxon:9606"
/clone="Plate=928 Col=17 Row=N"
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High quality sequence stop: 696

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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   DNA Sequencing by: Incyte Genomics, Inc.
Clone distribution: MGC clone distribution information can
found through the I.M.A.G.E. Consortium/LLNL at:
http://image.llnl.gov
Plate: LLAM9735 row: i column: 09
                                                                                                                                                                                                                      Contact: Robert Strausberg, Ph.D. Email: cgapbs-r@mail.nih.gov
Tissue Procurement: ATCC
                                                                                                                                                                                                                                                                                                                           Eukaryota; Metazoa; Chordata;
Mammalia; Eutheria; Primates;
1 (bases 1 to 835)
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EST.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  601512637F1 NIH_MGC_71 Homo
                                                                                                                                                                                                                                                                             Unpublished (1999)
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National Institutes of Health, Mammalian Gene Collection (MGC)
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          /clone="IMAGE:3849343"
/clone_lib="NIH MGC 65"
/tissue_type="adenocarcinoma"
/tissue_type="adenocarcinoma"
/lab_host="DH10B (phage-resistant)"
/note="Organ: colon; Vector: pCMV-SPORT6; Site_1: NotI;
Site_2: Sall; Cloned unidirectionally. Primer: Oligo dT.
Average insert size 1.8 kb. Library constructed by Life Technologies. "
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259 c 235 g
                 /organism≈"Homo sapiens"
/db_xref="taxon:9606"
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/db_xref="taxon:9606"
lone="IMAGE:3914192"
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Pred. No. 0.00
0; Mismatches
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National Institutes of Health, Mammalian
Unpublished (1999)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Mammalia; Eutheria; Primates; Catarrhini; Hominidae; 1 (bases 1 to 888)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              603180811F1 NIH_MGC_121
                                                                                                                                                                                                                                                                                                                                  DNA Sequencing by: Incyte Genomics, Inc.

Clone distribution: MGC clone distribution information can found through the I.M.A.G.E. Consortium/LLNL at:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Email:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Contact: Robert Strausberg, Ph.D.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Homo sapiens
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        BI919047.1
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BI919047
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                                                                                                                                                                                                                                                                                                                   http://image.llnl.gov
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                                                                                                                                                                                                                                                      quality sequence stop: 833.
Location/Qualifiers
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                     cgapbs-r@mail.nih.gov
                 /note="Organ: brain; Vector: pCMV-SPORT6; Site_1: Not1; Site_2: EcoRV (destroyed); RNA source anonymous pool of 3 fetal brains, female age 20 weeks, female age 24 weeks, and male age 26 weeks. Library is oligo-dT primed and directionally cloned (EcoRV site is destroyed upon
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             /lab_host="DH10B (phage-resistant)"
/note="Organ: uterus; Vector: pCMV-SPORT6; Site 1: Not1;
Site_2: Sal1; Cloned unidirectionally. Primer: Oligo dT.
Average insert size 2.1 kb. "
a 284 c 267 g 145 t
                                                                                                                       /db_xref="taxon:9606"
/clone="IMAGE:5245034"
/clone_lib="NIH_MGC_121"
/lab_host="DH10B"
                                                                                                                                                                                                          organism="Homo sapiens"
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Pred. No. 0.0046;
0; Mismatches 129;
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Best Local
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                                                                                                                                                                                                                                                                                                                                                                                                                                  PUBMED
Shibata, K., Itoh, M., Aizawa, K., Nagaoka, S., Sasaki, N., Carninci, P., Konno, H., Akiyama, J., Nishi, K., Kitsana, T., Tashiro, H., Itoh, M., Sumi, N., Ishii, Y., Nakamura, S., Hazama, M., Nishine, T., Harada, A., Yamamoto, R., Matsumoto, H., Sakaguchi, S., Ikegami, T., Kashiwagi, K., Fujiwake, S., Inoue, K., Togawa, Y., Izawa, M., Ohara, E., Watshiki, M., Yoneda, Y., Ishikawa, T., Ozawa, K., Tanaka, T., Matsuura, S., Kawai, J., Okazaki, Y., Muramatsu, M., Inoue, Y., Kira, A. and Hayashizaki, Y., RIKEN integrated sequence analysis (RISA) system-384-format sequencing pipeline with 384 multicapillary sequencer Genome Res. 10 (11), 1757-1771 (2000)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              516
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                                                                                                                                                                                                                                                                               Itoh, M., Konno, H., Okazaki, Y., Muramatsu, M. and Hayashizaki, Y. Muramatsu, M. and Hayashizaki, Y. Mormalization and subtraction of cap-trapper-selected cDNAs to prepare full-length cDNA libraries for rapid discovery of new genes Genome Res. 10 (10), 1617-1630 (2000)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Carninci, P. and Hayashizaki, Y.
High-efficiency full-length cDNA cloning
Meth. Enzymol. 303, 19-44 (1999)
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950 bp mRNA linear HTC 19-JAN-2002 Mus musculus 10 day old male pancreas cDNA, RIKEN full-length enriched library, clone:1810021F21:fibroblast growth factor 21,
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53.8%;
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Pred. No. 0.0045;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Kanagawa 230-0045, Japan (E-mail:genome-res@gsc.riken.go.jp, URL:http://genome.gsc.riken.go.jp/, Tel:81-45-503-9222, Fax:81-45-503-9216)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Direct Submission
Submitted (10-JUL-2000) Yoshihide Hayashizaki, The Institute of Physical and Chemical Research (RIKEN), Laboratory for Genome
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                                                                                                    /organism="Mus musculus"
/strain="C57BL/GJ"
/db_xref="FANTOM_DB:1810021F21"
/db_xref="MGD:MGT:1901172"
/db_xref="taxon:10090"
/clone="1810021F21"
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/tissue_type="pancreas"
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              CDNA Library Preparation: Ling Hong/Rubin Laboratory CDNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL) DNA Sequencing by: NIH Intramural Sequencing Center Clone distribution: MGC clone distribution information can found through the I.M.A.G.E. Consortium/LLNL at: http://image.llnl.gov Plate: LLCM1235 row: a column: 16
                                                                                                                                                                Tissue Procurement: ATCC
                                                                                                                                                                                                                          NIH-MGC http://mgc.nci.nih.gov/.
National Institutes of Health, N
Unpublished (1999)
                                                                                                                                                                                                                                                                                                                                                   Homo sapiens
                                                                                                                                                                                 Email: cgapbs-r@mail.nih.gov
                                                                                                                                                                                                   Contact: Robert Strausberg, Ph.D
                                                                                                                                                                                                                                                                                                   Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
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GPVRFLPMPGLLHEPQDQAGFLPPEPPDVGSSDPLSMVEPLQGR8PSYAS"
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/db_xref="G1:12841203"
/db_xref="G1:12841203"
/db_xref="MGD:MG1:1861377"
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/translation="MEMMRSRVGTLGLWVRLLLAVFLLGVYQAYPIPDSSPLLQFGGQ
/translation="MEMMRSRVGTLGLWVRLLLAVFLLGVYQAYPIPDSSPLLQFGGQ
/TRANSLYTDDDQDTBAHLEIRBDGTVVGAAHRSPBSLLELKALKPGVIQILGVKASRF
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/dev_stage="10 day old"
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    - Web: www.genoscope.cns.fr)
Determination of this BAC-end sequence was carried out as part collaboration with the Berkeley Drosophila Genome Project (BDGP)
The BDGP is constructing a physical map of the Drosophila melanogaster genome using these BACs. For further information please see http://www.fruitfly.org The BDGP Drosophila melanogaster BAC library was prepared by Kazutoyo Osoegawa and Aaron Mammoser in Pieter de Jong's laboratory in the Department Cancer Genetics at the Roswell Park Cancer Institute in Buffalo, NY. The library is named RPCI-98 and was concerned to
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             fly), gen
AL053013
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Direct Submission
Submitted (02-JUN-1999) Genoscope - Centre National de Sequencage
The sequencage of 191 91006 EVRY cedex - FRANCE (E-mail : seqref@genoscope.cns.fr
                                                                                                                                                                                                                                                                                                                                         Eukaryota; Metazoa; Arthropoda; Hexapoda; Insecta; Pterygota;
Neoptera; Endopterygota; Diptera; Brachycera; Muscomorpha;
Ephydroidea; Drosophilidae; Drosophila.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   UNSUUSIP 925 bp DNA linear GSS 03-JUN-1999 Drosophila melanogaster genome survey sequence TET3 end of BAC # BACR19D16 of RPCI-98 library from Drosophila melanogaster (fruit
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Drosophila melanogaster
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Genetics at the Roswell Park Cancer Institute in Buffalo
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/lab_host="DH10B (phage resistant)"
/note="Organ: colon; Vector: pOTB7; Site 1: XhoI; Site 2
ECORI; CDNA made by oligo-dr priming. Directionally cloned into EcoRI/XhoI sites using the following 5; adaptor: GGCACGAG(G). Size-selected >500bp for average insert size 1.8kb. Library constructed by Ling Hong in the laboratory of Gerald M. Rubin (University of California, Berkeley) using ZAP-CDNA synthesis kit (Stratagene) and Superscript II RT (Life Technologies)"
a 247 c 227 g 119 t
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/clone_lib="NIH_MGC_15"
/clssue_type="adenocarcinoma_cell
/clssue_type="adenocarcinoma_cell
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- Web: www.genoscope.Cns.fr)

Determination of this BAC-end sequence was carried out as part collaboration with the European Drosophila Genome Project (EDGP http://www.edgp.ebi.ac.uk - This Drosophila melanogaster BAC library (Dros BAC) was made by Alain Billaud at CEPH (Centre
                                                                                                                                                                                                                                                                                                                                                            Drosophila melanogaster genome sur
BACN15A08 of DrosBAC library from
fly), genomic survey sequence.
                                                                                                Submitted (23-JUL-1999) Genoscope - Centre BP 191 91006 EVRY cedex - FRANCE (E-mail:
                                                                                                                                                                                                 Drosophila melanogaster
Eukaryota; Metazoa; Arthropoda; Hexapoda; Insecta; Pterygo
Neoptera; Endopterygota; Diptera; Brachycera; Muscomorpha;
Ephydroidea; Drosophilidae; Drosophila.
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                                                                                                                                              Direct Submission
                                                                                                                                                                                                                                                                                    Drosophila melanogaster.
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/db xref="taxon:727"
/clone="BARR19D16"
/clone lib="RPCI-98"
/note="end : TET3"
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               81;
                                                                                                                                                      Email: est@watson.wustl.edu
This clone is available through: ResGen, Invitro
South Memorial Parkway Huntsville, AL 35801 For
                                                                                                                                                                                                                                                                                                                                                                                   Shoemaker, R., Keim, P., Vodkin, L., Erpelding, J., Coryell, V., Khanna, A., Bolla, B., Marra, M., Hillier, L., Kucaba, T., Martin, J., Beck, C. Wylie, T., Underwood, K., Steptoe, M., Theising, B., Allen, M., Bowers, Y., Person, B., Swaller, T., Gibbons, M., Pape, D., Harvey, N., Schurk
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and Gene
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta; Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots; Rosidae; eurosids I; Fabales; Fabaceae; Papilionoideae; Phaseoleae
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Glycine max
                                                                                                                                         call: (800)-533-4363 or contact via
                                                                                                                                                                                                              Tel: 314 286 1800
Fax: 314 286 1810
                                                                                                                                                                                                                                             Washington University School of Medicine
                                                                                                                                                                                                                                                                                   Contact: Shoemaker R/Public Soybean Public Soybean EST Project
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                                                                                                         quality sequence stop:
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/clone_lib="DrosBAC"
/plasmid="pBeloBAC11"
/note="end : T7"
                                  /organism="Glycine max"
/db_xref="taxon:3847"
/clone="GENOME SYSTEMS
/clone_lib="Gm-c1016"
                                                                                        Location/Qualifiers
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                     ID:
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                                                                                                                                                        Invitrogen Corp. 2130
801 For further information
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                   Gm-c1016-4042"
                                                                                                                                         ccu@resgen.com
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ionoideae; Phaseoleae;
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RESULT 14
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                                                                                      source
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Bukaryota; Metazoa; Arthropoda; Hexapoda; Insecta; Pterygota;
Neoptera; Endopterygota; Diptera; Brachycera; Muscomorpha;
Ephydroidea; Drosophilidae; Drosophila.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    GSS
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BACR14K09 of RPCI-98 library from
                                                                                                                                                                                                                                                                                                                                                                                                                                                                Submitted (02-JUN-1999) Genoscope - Centre National de Sequencage BP 191 91006 EVRY cedex - FRANCE (E-mail : segref@genoscope.cns.fr
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     AL065765
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                                                                                                                         http://bacpac.med.buffalo.edu/drosophila_bac.htm.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             // note-"Vector: pBluescript II XR; Site 1: EcoRI; Site 2: XhoI; This cDNA library was constructed from mRNA isolated from immature flowers of field grown plants. The cDNA library was prepared using the Stratagene pBluescript II XR library construction kit. Complementary DNA was
/organism="Drosophila melanogaster"
/db_xref="taxon:7227"
/clone="BACR14K09"
/clone_lib="RPCI-98"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            pBluescript vector. The ligated cDNA fragments were transformed into XL10-Gold host cells. This library was constructed by Dr. Randy Shoemaker and Dr. John Erpelding."
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          synthesized from mRNA using a primer consisting of a poly (dT) sequence with a XhoI restriction site. EcoRI adapters were ligated to the blunt-ended cDNA fragments followed by XhoI digestion. The cDNA fragments were directionally cloned into the EcoRI.XhoI restriction site of the
                                                                                                     Location/Qualifiers
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/lab_host="XL10-Gold"
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rom Drosophila melanogaster (fruit
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                segref@genoscope.cns.fr
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REFERENCE AUTHORS

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                                                                                                                     Query Match
Best Local Similarity
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                                  701 SBCCCKGTCKSCCCCCCTCTCMCCCCCYCCMKCRCKYYMTGKKTHMKMYMBMKKMMKMCK 642
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                                                                                                                                                                                                                                                                                                                                                                                                                          - Web: www.genoscope.cns.fr)
Determination of this BAC-end sequence was carried out as part collaboration with the European Drosophila Genome Project (EDC http://www.edgp.ebi.ac.uk - This Drosophila melanogaster BAC http://www.edgp.ebi.ac.uk - This Drosophila melanogaster BAC hibrary (Dros BAC) was made by Alain Billaud at CEPH (Centre
                                                                                                                                                                                                                                                                                                                                                          pBeloBAC11
                                                                                                                                                                                                                                                                                                                                                                        d'Etude du Polymorphisme Humain) with funding provided by a MRC project grant. The DNA was prepared from embryos by Alain Bucheton and Genevieve Payan. It has been constructed in the vector
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Eukaryota; Metazoa; Arthropoda; Hexapoda; Insecta; Pterygota;
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Ephydroidea; Drosophilidae; Drosophila.
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Patent No. US20020102604A1
GENERAL INFORMATION:
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Best Local Similarity
Matches 1239; Conser
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CURRENT FILING DATE: 2000-12-07
PRIOR APPLICATION NUMBER: US 60/169,629
PRIOR FILING DATE: 1999-12-08
PRIOR APPLICATION NUMBER: US 60/187,470
PRIOR FILING DATE: 2000-03-06
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      APPLICANT: Dumas Milne Edwards, Jean Baptist APPLICANT: Bougueleret, Lydie APPLICANT: Jobert, Severin TITLE OF INVENTION: FULL-LENGTH HUMAN cDNAs FILE REFERENCE: 78.US3.REG
                                                                                                                                                                                                                                                                                                                                                                                                                                           ORGANISM: Homo : FEATURE: NAME/KEY: CDS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          LENGTH: 1240
TYPE: DNA
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                    ATGAGCGTCCTCAGAGCCTATCCCAATGCCTCCCCACTGCTCGGCTCCAGCTGGGGTGGC
                                                                                   GGCACGATGTTGGGGGCCCGCCTCAGGCTCTGGGTCTGTGCCTTGTGCAGCGTCTGCAGC
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                                                               GECACGATGTTGGGGGCCCGCCTCAGGCTCTGGGTCTGTGCCTTGTGCAGCGTCTGCAGC
                                                                                                                             GCCAGGAGAGTCCCGACAGGAGTGTCAGGTTTCAATCTCAGCACCAGCCACTCAGAGCAG
                                                                                                                                                   GCCAGGAGAGTCCCGACAGGAGTGTCAGGTTTCAATCTCAGGCACCAGCCACTCAGAGCAG
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99.9%;
                                                                                                                                                                                                                                                           Score 1238.4;
Pred. No. 0;
0; Mismatches
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          CCTTCATGAAGGTAGAAGAGAGGGGTCTCTCCCAACATATTTCTCTTTCCTTGTGCCTCT
                                                    CCCTTCATGAAGGTAGAGAGAGGGGTCTCTCCCAACATATTTCTCTTCCTTGTGCCTCT
                                                                                                CTCACTCCATATAGAACACCTTTCCCAATAGGAAACCCCAACAGGTAAACTAGAAATTTC
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RESULT 3 US-09-924-340-25 Sequence 25, Application US/09924340 ; Publication No. US20030027248A1

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I LOCATION: 1..126

I NAME/KEY: CDS

LOCATION: 127..879

NAME/KEY: 3'UTR

LOCATION: 880..1239

NAME/KEY: polyA_site

LOCATION: 1224..1239

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CURRENT FILING DATE: 2001-08-06
PRIOR APPLICATION NUMBER: US 60/305,456
PRIOR FILING DATE: 2001-07-13
PRIOR APPLICATION NUMBER: US 60/302,277
PRIOR FILING DATE: 2001-06-29
PRIOR APPLICATION NUMBER: US 60/298,698
PRIOR APPLICATION NUMBER: US 60/293,574
PRIOR APPLICATION NUMBER: US 60/293,574
PRIOR APPLICATION NUMBER: US 60/293,574
PRIOR FILING DATE: 2001-05-25
NUMBER OF SEQ ID NOS: 112
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Query Match
Best Local Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   SOFTWARE: JI
SEQ ID NO 25
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APPLICANT: Tanaka, Hiroaki
TITLE OF INVENTION: HUMAN CDNAS AND PROTEINS AND USES THEREOF
FILE REFERENCE: 91.US2.REG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             ORGANISM: Homo sapiens FEATURE: NAME/KEY: 5'UTR
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TYPE: DNA
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                          ACGCTGGAAAACGGGTACGACGTCTACCACTCTCCTCAGTATCACTTCCTGGTCAGTCTG
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CTGATCCACCTGTACACAGCCACAGCCAGGAACAGCTACCACCTGCAGATCCACAAGAAT
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Pred. No. 0;
0; Mismatches
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APPLICANT: Benjanin, Stephane
APPLICANT: Benjanin, Stephane
APPLICANT: Tanaka, Hiroaki
FIIIE OF INVENTION: HUMAN CDNAS AND PROTEINS ANI
FILE REFERENCES: 91 US4.DIV
CURRENT APPLICATION NUMBER: US/09/992,600A
CURRENT FILING DATE: 2001-08-06
PRIOR FILING DATE: 2001-08-06
PRIOR PRILING DATE: 2001-08-06
PRIOR APPLICATION NUMBER: PCT/IB01/01715
PRIOR APPLICATION NUMBER: US/03/05,456
PRIOR APPLICATION NUMBER: US/03/05,456
PRIOR FILING DATE: 2001-07-13
PRIOR APPLICATION NUMBER: US/03/02,277
PRIOR APPLICATION NUMBER: US/03/02,277
PRIOR FILING DATE: 2001-06-29
PRIOR APPLICATION NUMBER: US/03/02,277
PRIOR APPLICATION NUMBER: US/03/02,277
PRIOR APPLICATION NUMBER: US/03/02,277
PRIOR FILING DATE: 2001-06-15
PRIOR APPLICATION NUMBER: US/03/02,574
PRIOR FILING DATE: 2001-05-25
NUMBER OF SEQ ID NOS: 114
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NAME/KEY: polyA_site
LOCATION: 1224..1239
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LOCATION: 127..879
FEATURE:
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LOCATION: 1..126
FEATURE:
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ORGANISM: Homo sapiens
FEATURE:
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LOCATION: 880..1239
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RESULT 4 US-09-992-600A-25

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Sequence 25, Application US/09992600A publication No. US20030027161A1 GENERAL INFORMATION:

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CURRENT APPLICATION NUMBER: US/10/000,489
CURRENT FILING DATE: 2001-11-14
PRIOR APPLICATION NUMBER: US 09/924,340
PRIOR APPLICATION NUMBER: US 09/924,340
PRIOR APPLICATION NUMBER: PCT/IB01/01715
PRIOR FILING DATE: 2001-08-06
PRIOR FILING DATE: 2001-08-07
PRIOR PILING DATE: 2001-07-13
PRIOR PILING DATE: 2001-07-13
PRIOR FILING DATE: 2001-06-29
PRIOR FILING DATE: 2001-06-29
PRIOR FILING DATE: 2001-06-29
PRIOR FILING DATE: 2001-06-15
PRIOR FILING DATE: 2001-06-15
PRIOR FILING DATE: 2001-05-25
NUMBER OF SEQ ID NOS: 112
SOFTWARE: JPAtent
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Publication No. US20030092011A1

GENERAL INFORMATION:

APPLICANT: Benjannin, Stephane

APPLICANT: Tanaka, Hiroaki

TITLE OF INVENTION: HUMAN CDNAS AND PROTEINS AND USES THEREOF

FILE REFERENCE: 91 US6.DIV
                                                                                                                                                                                                                 SEQ ID NO 25
LENGTH: 1239
TYPE: DNA
ORGANISM: Homo sapiens
FEATURE:
NAME/KEY: 5'UTR
LOCATION: 1.126
NAME/KEY: CDS
LOCATION: 127.879
NAME/KEY: 3'UTR
LOCATION: 880.1239
NAME/KEY: polyA site
LOCATION: 1224.1239
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CURRENT APPLICATION NUMBER: US/09/754,634A
CURRENT FILLING DATE: 2001-05-11
PRIOR APPLICATION NUMBER: US 60/174,582
PRIOR FILING DATE: 2000-01-05
NUMBER OF SEQ ID NOS: 6
SOPTWARE: PASTSEQ for Windows Version 4.0
SEQ ID NO 1
LENGTH: 1211
TYPE: DNA
ORGANISM: Homo sapiens
FEATURE:
NAME/KEY: CDS
LOCATION: (115)...(870)
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TITLE OF INVENTION: FGF HOMOLOG ZFGF12
FILE REFERENCE: 00-02
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                   Sequence 510, Application US/09992598
Patent NO. US20020160384A1
GENERAL INFORMATION:
APPLICANT: Ashkenazi, Avi J.
APPLICANT: Baker, Kevin P.
APPLICANT: Betstein, David
APPLICANT: Betstein, David
APPLICANT: Betsoyers, Luc
APPLICANT: Eston, Dan L.
APPLICANT: Ferrara, Napoleone
APPLICANT: Ferrara, Napoleone
APPLICANT: Gerber, Hanspeter
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Gerber, Hanspeter
Gerritsen, Mary E.
Goddard, Audrey
Godowski, Paul J.
Grimaldi, J. Christopher
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PRIOR PILING DATE: 1997-10-17
PRIOR APPLICATION NUMBER: 60/065186
PRIOR FILING DATE: 1997-11-12
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PRIOR FILING DATE: 1997-06-16
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CURRENT FILING DATE: 2001-11-14
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TITLE OF INVENTION: Secreted and Transmembrane Polypeptides and Nucleic
TITLE OF INVENTION: Acids Encoding the Same
FILE REFERENCE: P2730P1C20
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APPLICATION NUMBER: 60/088655
FILING DATE: 1998-06-09
APPLICATION NUMBER: 60/088734
FILING DATE: 1998-06-10
                                                                  FILING DATE: 1998-06-05
                                                                                APPLICATION NUMBER: 60/088217
                                                                                                   APPLICATION NUMBER: 60/088212 FILING DATE: 1998-06-05
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FILING DATE: 1998-06-05
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FILING DATE: 1998-06-04
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APPLICATION NUMBER: 60/088030
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APPLICATION NUMBER: 60/088029
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APPLICATION NUMBER: 60/088026
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APPLICATION NUMBER: 60/088025
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APPLICATION NUMBER: 60/087827
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APPLICATION NUMBER: 60/087759
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APPLICATION NUMBER: 60/087609
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Kljavin,Ivar J.
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OR FILLING DATE: 1998-06-16

OR PPLICATION NUMBER: 60/089532

OR FILLING DATE: 1998-06-17

OR APPLICATION NUMBER: 60/089538

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TITLE OF INVENTION: Acids Encoding the Same
FILE REFERENCE: P2730P1C66
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Williams, P. Mickey
Wood, William I.
Zhang, Zemin
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Stewart, Timothy A.
Tumas, Daniel
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Grimaldi, J. Christopher
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Gerritsen, Mary E
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Eaton, Dan L.
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DR APPLICATION NUMBER: 60/088025
DR FILING DATE: 1998-06-04
DR APPLICATION NUMBER: 60/088026
DR FILING DATE: 1998-06-04
DR APPLICATION NUMBER: 60/088028
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APPLICATION NUMBER: 60/087609 FILING DATE: 1998-06-02 APPLICATION NUMBER: 60/087759 FILING DATE: 1998-06-02 APPLICATION NUMBER: 60/087827

FILING DATE: 1998-06-03
APPLICATION NUMBER: 60/088021
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APPLICATION NUMBER: 60/087607
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APPLICATION NUMBER: 60/084600
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APPLICATION NUMBER: 60/083322
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OR APPLICATION NUMBER: 60/091978
OR FILING DATE: 1998-07-07
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PRIOR FILING DATE: 1997-06-16
PRIOR PELICATION NUMBER: 60/06250
PRIOR PILING DATE: 1997-10-17
PRIOR APPLICATION NUMBER: 60/065186
PRIOR FILING DATE: 1997-11-12
PRIOR APPLICATION NUMBER: 60/065311
PRIOR PILING DATE: 1997-11-13
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CURRENT APPLICATION NUMBER: US/09/989,735
CURRENT FILING DATE: 2001-11-19
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APPLICATION NUMBER: 60/088030
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APPLICATION NUMBER: 60/
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Kljavin, Ivar J.
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Grimaldi,J.Christopher
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Gerritsen, Mary E
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114 AATCTCAGCACCAGCCACTCAGAGCAGGGCACGATGTTGGGGGCCCCGCCTCAGGCTCTGG 173 319 199 AATCTCAGCACCAGCCACTCAGAGCAGGGCACGATGTTGGGGGGCCCGCCTCAGGCTCTGG CCACTGCTCGGCTCCAGCTGGGGTGGCCTGATCCACCTGTACACAGCCACAGCCAGGAAC 293 GTCTGTGCCTTGTGCAGCGTCTGCAGCATGAGCGTCCTCAGAGCCTATCCCCAATGCCTCC 233 CCACTGCTCGGCTCCAGCTGGGGTGGCCTGATCCACCTGTACACAGCCACAGCCAGGAAC GTCTGTGCCTTGTGCAGCGTCTGCAGCGTCCTCAGAGCCTATCCCAATGCCTCC Length 996 Indels 0; Gaps 378 258 318 0

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60/090349 60/090254 60/090252 FILING DATE: 1998-06-19 APPLICATION NUMBER: 60/089952

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Baker, Kevin P.
Botstein, David
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Gerber, Hanspeter
Gerritsen, Mary E.
Goddard, Audrey
Godowski, Paul J.
Grimaldi, J. Christopher
Watanabe, Colin
Williams, P. M.
Wood, William
                                                      Stewart, Timo
Tumas, Daniel
                                                                                                                                                                        Gurney, Austin L.
Kljavin, Ivar J.
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Eaton, Dan L.
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                                                                                                                  Paoni,Nicholas F.
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                                                                        Margaret Ann
art, Timothy A.
                  Colin K.
P. Mickey
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OR APPLICATION NUMBER: 60/075945
OR FILING DATE: 1998-02-25
OR APPLICATION NUMBER: 60/078910
OR FILING DATE: 1998-03-20
OR APPLICATION NUMBER: 60/083322
OR APPLICATION NUMBER: 60/084600
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OR FILING DATE: 1998-06-03
OR PELLING DATE: 1998-06-04
OR APPLICATION NUMBER: 60/088021
OR APPLICATION NUMBER: 60/088025
OR FILING DATE: 1998-06-04
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FILING DATE: 1998-05-28
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CURRENT APPLICATION NUMBER: US/09/990,444
CURRENT FILING DATE: 2001-11-14
PRIOR APPLICATION NUMBER: 60/049787
                                                                                  APPLICANT: Zhang, Zemin
TITLE OF INVENTION: Secreted and Transmembrane Polypeptides and Nucleic
TITLE OF INVENTION: Acids Encoding the Same
FILE REFERENCE: P2730P1C19
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PR FILING DATE: 1998-06-24

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DR FILING DATE: 1998-06-17
DR APPLICATION NUMBER: 60/089801
DR FILING DATE: 1998-06-18
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DR APPLICATION NUMBER: 60/090535
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OR APPLICATION NUMBER: 60/091519
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PRIOR FILING DATE: 1997-10-17 PRIOR FILING DATE: 1997-11-12 PRIOR APPLICATION NUMBER: 60/065186 PRIOR PRILING DATE: 1997-11-13 PRIOR APPLICATION NUMBER: 60/066770 PRIOR PILING DATE: 1997-11-24 PRIOR APPLICATION NUMBER: 60/075945 PRIOR PILING DATE: 1997-11-24 PRIOR APPLICATION NUMBER: 60/075945 PRIOR PILING DATE: 1998-02-25 PRIOR APPLICATION NUMBER: 60/078910 PRIOR PILING DATE: 1998-03-20 PRIOR APPLICATION NUMBER: 60/083322 PRIOR APPLICATION NUMBER: 60/083322 PRIOR APPLICATION NUMBER: 60/08700 PRIOR APPLICATION NUMBER: 60/087106 PRIOR APPLICATION NUMBER: 60/087607 PRIOR APPLICATION NUMBER: 60/087607 PRIOR APPLICATION NUMBER: 60/087607	CANT: Gurney, Austin L. CANT: Rijavin, Ivar J. CANT: Napier, Mary A. CANT: Pan, James CANT: Pan, James CANT: Pan, James CANT: Pan, James CANT: Roy, Margaret Ann CANT: Stewart, Timothy A. CANT: Watanabe, Colin K. CANT: Williams, P. Mickey CANT: Williams, P. Mickey CANT: Wood, William I. CANT: Zhang, Zemin OF INVENTION: Secreted and Transmembrane Polypeptides OP INVENTION: Acids Encoding the Same REPERENCE: P2730P1C69 NT FILING DATE: 2001-11-20 NT FILING DATE: 1997-06-16 APPLICATION NUMBER: 60/049787 FILING DATE: 1997-06-16 APPLICATION NUMBER: 60/062250	10, pp N N N N N N N N N N N N N N N N N N	OY 714 CTGAACGTGCTGAAGCCCCGGGCCCGGATGACCCCGGCCCCGGCCTCCTGTTCACAGGAG
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RESULT 12
US-09-990-436-510
; Sequence 510, Application US/;
; Publication No. US20020198148;
; CENERAL INFORMATION:
; APPLICANT: Baker, Kevin P.
; APPLICANT: Botstein, David
; APPLICANT: Desnoyers, Luc
; APPLICANT: Eaton, Dan L. Ferrara, Napoleone

PRIOR PRIOR

R PILING DATE:
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NUMBER:

NUMBER: 60/091982 1998-07-07

N NUMBER: 60/091633 E: 1998-07-02 N NUMBER: 60/091978 E: 1998-07-07

NUMBER: 60/091626: 1998-07-02

60/091519

DR FILING DATE: 1998-06-26
DR APPLICATION NUMBER: 60/09
DR FILING DATE: 1998-06-26
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1998-07-02 NUMBER: 60/091544

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DR FILING DATE: 1998-06-25

RAPPLICATION NUMBER: 60/090678

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DR FILING DATE: 1998-06-24

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DR FILING DATE: 1998-06-24

DR APPLICATION NUMBER: 60/090542

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DR APPLICATION NUMBER: 60/090557

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1998-06-24

APPLICATION NUMBER: 60/090444 FILING DATE: 1998-06-24

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FILING DATE: 1998-06-19 APPLICATION NUMBER: 60/089948

NUMBER: 60/089947

NUMBER: 60/089908

1998-06-18

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FILING DATE: APPLICATION I APPLICATION

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CURRENT FILING DATE: 2001-11-14
PRIOR APPLICATION NUMBER: 60/049787
PRIOR FILING DATE: 1997-06-16
PRIOR APPLICATION NUMBER: 60/062250
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ITTLE OF INVENTION: Secreted and Transmembrane Polypeptides and Nucleic TITLE OF INVENTION: Acids Encoding the Same FILE REPERENCE: P2730PIC14

CURRENT APPLICATION NUMBER: US/09/990,436

CURRENT FILING DATE: 2001-11-14
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DR FILING DATE: 1998-06-04

DR APPLICATION NUMBER: 60/088167

DR PILING DATE: 1998-06-05

DR APPLICATION NUMBER: 60/088202
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PR APPLICATION NUMBER: 60/087827
PR FILLING DATE: 1998-06-03
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APPLICATION NUMBER: 60/078910
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Gerber, Hanspeter
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Williams, P. Mickey
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DR APPLICATION NUMBER: 60/090676

DR FILING DATE: 1998-06-25

DR APPLICATION NUMBER: 60/090694
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APPLICATION NUMBER: 60/091982
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APPLICATION NUMBER: 60/092182
FILING DATE: 1998-07-09
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APPLICATION NUMBER: 60/091633
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APPLICATION NUMBER: 60/090695
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APPLICATION NUMBER: 60/090557
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APPLICATION NUMBER: 60/090540
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APPLICATION NUMBER: 60/090472
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APPLICANT: Watanabe, Colin K.
APPLICANT: Wolliams, P. Mickey
APPLICANT: Williams, P. Mickey
APPLICANT: Wood, William I.
APPLICANT: Zhang, Zemin
TITLE OF INVENTION: Secreted and Transmembrane Pol
TITLE OF INVENTION: Acids Encoding the Same
FILE REFERENCE: P2730P1C53
CURRENT APPLICATION NUMBER: US/09/991,181
CURRENT FILING DATE: 2001-11-16
PRIOR APPLICATION NUMBER: 60/049787
PRIOR FILING DATE: 1997-06-16
PRIOR APPLICATION NUMBER: 60/062250
PRIOR APPLICATION NUMBER: 60/065186
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Stewart, i....
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Roy, Margaret Ann
Stewart, Timothy A.
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Kljavin, Ivar J.
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Grimaldi, J. Christopher
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DR FILING DATE: 1997-11-12
DR APPLICATION NUMBER: 60/065311
DR FILING DATE: 1997-11-13
DR APPLICATION NUMBER: 60/066770
DR FILING DATE: 1997-11-24
DR APPLICATION NUMBER: 60/075945
DR FILING DATE: 1998-02-25
DR FILING DATE: 1998-02-25

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OR APPLICATION NUMBER: 60/08322
OR FILING DATE: 1998-03-20
OR APPLICATION NUMBER: 60/083322
OR APPLICATION NUMBER: 60/083322
OR APPLICATION NUMBER: 60/084600
OR FILING DATE: 1998-05-07
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OR APPLICATION NUMBER: 60/087609
OR FILING DATE: 1998-06-02
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OR APPLICATION NUMBER: 60/088876
OR FILING DATE: 1998-06-11
OR APPLICATION NUMBER: 60/089105
OR FILING DATE: 1998-06-12
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DR FILING DATE: 1998-07-02
DR APPLICATION NUMBER: 60/091633
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DR APPLICATION NUMBER: 60/991978
DR FILING DATE: 1998-07-07
DR APPLICATION NUMBER: 60/091982
DR FILING DATE: 1998-07-07
DR APPLICATION NUMBER: 60/092182
DR FILING DATE: 1998-07-09
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APPLICATION NUMBER: 60/091519
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APPLICATION NUMBER: 60/091478
FILING DATE: 1998-07-02
APPLICATION NUMBER: 60/091544
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                               GGTCGAGTGAACACGCACGCTGGGGGAACGGCCCGGAAGGCTGCCGCCCCTTCGCCAAG
                                                                                    CTCCCGAGCGCCGAGGACAACAGCCCGATGGCCAGTGACCCATTAGGGGTTGGTCAGGGGC
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GENERAL INFORMATION:
APPLICANT: Ashkenazi, Avi J.
APPLICANT: Baker, Kevin P.
APPLICANT: Botstein, David
APPLICANT: Desnoyers, Luc
APPLICANT: Eaton, Dan L.
APPLICANT: Ferrara, Napoleon
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TITLE OF INVENTION: Secreted and Transmembra
TITLE OF INVENTION: Acids Encoding the Same
FILE REFERENCE: P2730P1C11
CURRENT APPLICATION NUMBER: US/09/93,687
CURRENT FILING DATE: 2002-11-14
PRIOR APPLICATION NUMBER: 60/049787
PRIOR FILING DATE: 1997-06-16
PRIOR APPLICATION NUMBER: 60/062250
PRIOR APPLICATION NUMBER: 60/065186
PRIOR APPLICATION NUMBER: 60/065186
PRIOR APPLICATION NUMBER: 60/065181
PRIOR APPLICATION NUMBER: 60/065311
PRIOR APPLICATION NUMBER: 60/065311
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R FILLING DATE: 1998-06-02

DR APPLICATION NUMBER: 60/087827

DR FILLING DATE: 1998-06-03

DR APPLICATION NUMBER: 60/088021

DR FILING DATE: 1998-06-04
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FILING DATE: 1998-06-02
APPLICATION NUMBER: 60/087609
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APPLICATION NUMBER: 60/087106
FILING DATE: 1998-05-28
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APPLICATION NUMBER: 60/088025
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Williams, P. Mickey
Wood, William I.
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Goddard, Audrey
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Kljavin, Ivar J.
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Stewart, Timothy A.
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APPLICATION NUMBER: 60/091360
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                                                                                       Score 798; DB 9;
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FILING DATE: 1998-06-10 APPLICATION NUMBER: 60/088826 FILING DATE: 1998-06-10 APPLICATION NUMBER: 60/088858

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APPLICATION NUMBER: 60/088202 APPLICATION NUMBER: 60/088167 FILING DATE: 1998-06-05 FILING DATE: 1998-06-04

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Baker, Kevin P.
Botstein, David
                                                                                                                     Fong, Sherman
Gerber, Hanspeter
Gerritsen, Mary E.
Goddard, Audrey
                                                 Godowski, Paul J.
Grimaldi, J.Christopher
Gurney, Austin L.
Kljavin, Ivar J.
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   Paoni, Nicholas F
                                 Napier, Mary A.
                                                                                                                                                                                           Ferrara, Napoleone
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CURRENT APPLICATION NUMBER: US/09/989,734
CURRENT FILING DATE: 00/049787
PRIOR FILING DATE: 1997-06-16
PRIOR FILING DATE: 1997-06-16
PRIOR PILING DATE: 1997-06-16
PRIOR PILING DATE: 1997-10-17
PRIOR FILING DATE: 1997-10-17
PRIOR FILING DATE: 1997-11-12
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PRIOR APPLICATION NUMBER: 60/065311
PRIOR APPLICATION NUMBER: 60/065311
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PRIOR FILING DATE: 1998-04-28
PRIOR APPLICATION NUMBER: 60/084600
PRIOR FILING DATE: 1998-05-07
PRIOR APPLICATION NUMBER: 60/087106
PRIOR FILING DATE: 1998-05-28
PRIOR APPLICATION NUMBER: 60/087607
PRIOR FILING DATE: 1998-06-02
PRIOR FILING DATE: 1998-06-02
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PRIOR APPLICATION NUMBER: 60/66770
PRIOR FILING DATE: 1997-11-24
PRIOR APPLICATION NUMBER: 60/075945
PRIOR APPLICATION NUMBER: 60/075945
PRIOR APPLICATION NUMBER: 60/078910
PRIOR APPLICATION NUMBER: 60/078910
PRIOR FILING DATE: 1998-03-20
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OR APPLICATION NUMBER: 60/078910
OR FILING DATE: 1998-03-20
OR APPLICATION NUMBER: 60/083322
OR FILING DATE: 1998-04-28
OR APPLICATION NUMBER: 60/084600
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FILING DATE: 1998-06-04
APPLICATION NUMBER: 60/
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Williams, P. Micke
Wood, William I.
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Stewart, Timothy
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DR FILING DATE: 1998-06-10

PR APPLICATION NUMBER: 60/088824

PR APPLICATION NUMBER: 60/088826

PR APPLICATION NUMBER: 60/088826

PR FILING DATE: 1998-06-10

PR APPLICATION NUMBER: 60/088858

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APPLICATION NUMBER: 60/091633
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APPLICATION NUMBER: 60/091978
FILING DATE: 1998-07-07
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FILING DATE: 1998-07-07
APPLICATION NUMBER: 60/092182
FILING DATE: 1998-07-09
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APPLICATION NUMBER: 60/091478
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APPLICATION NUMBER: 60/091544
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APPLICATION NUMBER: 60/091626
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APPLICATION NUMBER: 60/090863
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APPLICATION NUMBER: 60/090694
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APPLICATION NUMBER: 60/
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APPLICATION NUMBER: 60/090862
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AACCCACCCCCGTACTCCCAGTTCCTGTCCCGGAGGAACGAGATCCCCCTAATTCACTTC
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                                                        CCTCAGTATCACTTCCTGGTCAGTCTGGGCCGGGCGAAGAGAGCCTTC
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PRIOR PRIOR

APPLICATION NUMBER: 60/089948 FILING DATE: 1998-06-19 APPLICATION NUMBER: 60/089952 FILING DATE: 1998-06-19

APPLICATION NUMBER: 60/ FILING DATE: 1998-06-22

FILING DATE: 1998-06-18
APPLICATION NUMBER: 60/089908
FILING DATE: 1998-06-18
APPLICATION NUMBER: 60/089947
FILING DATE: 1998-06-19

FILING DATE: 1998-06-18 APPLICATION NUMBER: 60/089907

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DR FILING DATE: 1998-06-17
DR APPLICATION NUMBER: 60/089538
DR FILING DATE: 1998-06-17
OR APPLICATION NUMBER: 60/089598
OR FILING DATE: 1998-06-17
DR APPLICATION NUMBER: 60/089599
DR FILING DATE: 1998-06-17
DR APPLICATION NUMBER: 60/089600
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FILING DATE: 1998-06-16
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APPLICATION NUMBER: 60/089532

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OR FILING DATE: 1998-06-11
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DR FILING DATE: 1998-06-11
DR APPLICATION NUMBER: 60/08876
DR FILING DATE: 1998-06-11
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FILING DATE: 1998-06-24

FILING DATE: 1998-06-23
APPLICATION NUMBER: 60/090355
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APPLICATION NUMBER: 60/090429

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60/090252 60/090246

APPLICATION NUMBER: 60/090349

APPLICATION NUMBER: 60/090542 FILING DATE: 1998-06-24 APPLICATION NUMBER: 60/090557 FILING DATE: 1998-06-24

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APPLICATION NUMBER: 60/090535 FILING DATE: 1998-06-24 APPLICATION NUMBER: 60/090540 FILING DATE: 1998-06-24

APPLICATION NUMBER: 60/090445
FILING DATE: 1998-06-24
APPLICATION NUMBER: 60/090472

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CCCC 713			GGAAGGCTGCCGCCCCTTCGCCAAG 978	GGAAGGCTGCCGCCCCTTCGCCAAG 893	TGACCCATTAGGGGTGGTCAGGGGC 918	TGACCCATTAGGGGTGGTCAGGGGC 833	GGCCCCGGCCTCCTGTTCACAGGAG 858	GGCCCCGGCCTCCTGTTCACAGGAG 773	CGAGGACGACTCGGAGCGGGACCCC 798	CGAGGACGÁCTCGGAGCGGGACCCC 713	GAACGAGATCCCCCTAATTCACTTC 738

Search completed: May 29, 2003, 00:05:38 Job time : 268 secs

Sequence 21, Appl Sequence 20, Appl Sequence 20, Appl Sequence 31, Appl Sequence 10, Appl Sequence 11, Appl Sequence 12, Appl Sequence 14, Appl Sequence 14, Appl Sequence 14, Appl Sequence 45, Appl Sequence 45, Appl Sequence 45, Appl Sequence 41, Appl Sequence 41,

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/cgn2_6/ptodata/1/ina/5B_COMB.seq:*
/cgn2_6/ptodata/1/ina/6A_COMB.seq:*
/cgn2_6/ptodata/1/ina/6B_COMB.seq:*
/cgn2_6/ptodata/1/ina/PCTUS_COMB.seq:*
/cgn2_6/ptodata/1/ina/backfiles1.seq:*
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US-09-484-9708-167
US-08-713-000-8
US-08-713-000-8
US-08-975-316-8
US-09-615-192A-8
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US-09-615-192A-93
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April 4 1988 April 4 1988 April 5 7/062,9 June 16, 1987 INFORMATION: M. Frankfort NUMBER: 32,613 CKET NUMBER: 598 ION INFORMATION: (212) 527-770 12) 753-6237 SEQ ID NO: 2: CTERISTICS: ic acid single inear Genomic DNA	US/08187780 ALARICO MAMMALIAN G B B SS: Darby P.C. Avenue Ette, 5.25 i tte, 5.25 i tte, 5.25 i US/08/187 US/08/187 OT/806,77 ber 6, 1991,70 Der 6, 1991	C 28 43.6 2.7 3131 3 US-09-146-249A-21 C 29 43.6 2.7 3131 3 US-08-206-188B-21 C 30 43.6 2.7 3131 5 PCT-US91-02714-20 C 31 43.6 2.7 7218 1 US-08-23-463-1 4 US-09-813-133A-3 3 43.2 2.7 3073 1 US-09-813-133A-3 3 43.2 2.7 3073 2 US-08-474-379C-31 35 43.2 2.7 3073 2 US-08-474-379C-31 35 43.2 2.7 3073 3 US-09-146-249A-31 37 43.2 2.7 3073 3 US-09-166-188B-31 37 43.2 2.7 3073 5 PCT-US91-02714B-30 38 43.2 2.7 3073 5 PCT-US91-02714B-31 42 42.6 2.6 624 4 US-09-359-860A-1 42 42.2 2.6 1159 4 US-09-370-83B-151 42 42 2.6 1159 4 US-09-370-83B-151 44 42 2.6 11517 4 US-08-466-277-1 45 42 2.6 11517 4 US-08-466-277-1

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Best Local Similarity
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         SOFTWARE: Wordperfect
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/187,780
                                                      COMPUTER READABLE FORM:
MEDIUM TYPE: Diskette, 5.25 inch,
MEDIUM TYPE: 360 Kb storage
COMPUTER: IBM or IBM-compatible
OPERATING SYSTEM: PC/MS-DOS
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IDENTIFICATION METHOD:
OTHER INFORMATION: Thi
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 FILING DATE:
                                                                                                                                                     COUNTRY:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                   ACTCTCCTCAGTATCACTTCCTGGTCA 555
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                                                                                                                                                                     New York
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DANIELA TALARICO
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January 25, 1994
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Pred. No. 0.00016;
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RELEVANT RESIDUES
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Best Local Similarity 52.4
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APPLICATION NUMBER: 07/062,925
FILING DATE: June 16, 1987
ATTORNEY/AGENT INFORMATION:
NAME: Howard M. Frankfort
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DESCRIPTION:
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                                                                                        469
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STRANDEDNESS: single
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            TITLE:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          AUTHORS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              REGISTRATION NUMBER: 32,613
REFERENCE/DOCKET NUMBER: 59
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AGTCCTACAAGTACCCCGGCATGTTCA 337
                            ACTCTCCTCAGTATCACTTCCTGGTCA
                                                            TCACC--
                                                                                   TCGACCCGGAGAACTGCAGGTTCCAACACCAGACGCTGGAAAAACGGGTACGACGTCTACC 528
                                                                                                                      TGGCCAGCCGGTTCTTCGTGGCCATGAGCAGCAAGGGCAAGCT
                                                                                                                                                TGATGAGCAGAAGATACCTCTGCATGGATTTCAGAGGCAACATTTTTGGATCACACTATT
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                                                        -GATGAGTGCACGTTCAAGGAGATTCTCCTTCCCAACAACTACAACGCCTACG
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Pred: No. 0.00016;
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APPLICANT: CLAUDIO
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NFORMATION FOR SEQ ID NO:
                                                                                                                                                                                                                                                                                                                                                           MOLECULE TYPE:
DESCRIPTION:
HYPOTHETICAL:
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ATTORNEY/AGENT INFORMATION:
NAME: Joseph R. Robinson
REGISTRATION NUMBER: 33,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         SEQUENCE CHARACTERISTICS:
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MEDIUM TYPE: Floppy Diskette,
MEDIUM TYPE: 1.44 MB storage
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APPLICANT: DANIELA TALARICO
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OTHER INFORMATION: Th
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OTHER INFORMATION: ap
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FILING DATE: April 4, 1988
APPLICATION NUMBER: 07/062,
FILING DATE: June 16, 1987
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APPLICATION NUMBER: 07/8
FILING DATE: December 6,
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APPLICATION NUMBER: 07/901,705
APPLICATION NUMBER: 07/901,705
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                  PUBLICATION DATE:
                                      FILING DATE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         CLASSIFICATION:
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STATE: New York
                                                       OCUMENT NUMBER:
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NUMBER: 07/806,771
December 6, 1991
NUMBER: 07/177,506
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IN SEQ ID NO:
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                                                                                                                                                                                                                              This sequence can be found on page 5, line
                                                                                                                                                                                                                 application,
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Best Local Similarity 52.4%;
Matches 140; Conservative
                                                                                                  APPLICATION NUMBER: 07/177,506
FILING DATE: April 4, 1988
APPLICATION NUMBER: 07/062,925
FILING DATE: June 16, 1987
ATTORNEY/AGENT INFORMATION:
NAME: Joseph R. Robinson
REGISTRATION NUMBER: 33,448
REFERENCE/DOCKET NUMBER: 3986/13:
TELECOMMUNICATION INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           APPLICANT: CLAUDIO BAPPLICANT: DANIELA TATITLE OF INVENTION: NUMBER OF SEQUENCES:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            PRIOR APPLICATION DATA:
APPLICATION NUMBER:
FILING DATE: January
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      SOFTWARE: Wordperfect
CURRENT APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy Diskette,
MEDIUM TYPE: 1.44 MB storage
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  529
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         311 AGTCCTACAAGTACCCCGGCATGTTCA 337
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                                                                                                                                                                                                                                                                                                                                                                                                                                              FILING DATE: June 22,
APPLICATION NUMBER: 07
FILING DATE: December
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THE TRANSPORT OF THE TRANSPOR
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OPERATING SYSTEM:
                                                                       TELEPHONE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           CLASSIFICATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       APPLICATION NUMBER: US/08/478,485 FILING DATE: Concurrently Herewith
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       COUNTRY: U
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805 Third Avenue
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(212) 753-6237
DR SEQ ID NO: |
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DANIELA TALARICO
ENTION: MAMMALIAN GROWTH FACTOR
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     IBM PC compatible SYSTEM: PC/MS-DOS
                                                                       (212)
                                                                       527-7700
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Pred. No. 0.00016;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Length 423;
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Best Local Similarity 52.4%;
Matches 140; Conservative
                                                                                                                                                                                                                                                                                          Sequence 2, Application US/08478486F Patent No. 6432702
                                                                                                                                                                  APPLICANT: CLAUDIO BASILICO
APPLICANT: DANIELA TALARICO
TITLE OF INVENTION: MAMMALIAN GROWTH
NUMBER OF SEQUENCES: 12
CORRESPONDENCE ADDRESS:
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy Diskette, 3+ inch,
MEDIUM TYPE: 1.44 MB storage
                                                                                                                                                                                                                                                                                                                                                                                                                 311
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DESCRIPTION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  74 GCATCGGCTTCCACCTCCAGGCGCTCCCCGACGGCCGCATCGGCGGCGCGCACGCGGACA 133
                                                                                                                                      STREET:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            FILING DATE:
PUBLICATION DATE:
RELEVANT RESIDUES IN SEQ ID NO: 1-423
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OTHER INFORMATION:
                                                                                                                    CITY: New York
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         TYPE: nucleic acid
STRANDEDNESS: single
TOPOLOGY: linear
                                                                                 COUNTRY:
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                                                                                                                                                            ADDRESSEE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    JOURNAL:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          AUTHORS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          IDENTIFICATION METHOD:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    NAME/KEY:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               TGGCCAGCCGGTTCTTCGTGGCCATGAGCAGCAAGCGCAAGCTCTATGGCTCGCCCTTCT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            CCATCTACAGTGCCCTGATGATCAGATCAGAGGATGCTGGCTTTGTGGTGATTACAGGTG 408
                                                                                                                                                                                                                                                                                                                                                                                                           AGTCCTACAAGTACCCCGGCATGTTCA 337
                                                                                                                                                                                                                                                                                                                                                                                                                                               ACTCTCCTCAGTATCACTTCCTGGTCA 555
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   TGATGAGCAGAAGATACCTCTGCATGGATTTCAGAGGCAACATTTTTGGATCACACTATT 468
                                                                                                                                                                                                                                                                         INFORMATION:
                                                             10022
                                                                                                  New York
                                                                                                                                      E: Darby & Darby P.C
805 Third Avenue
                                                                               USA
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Corresponds to K-FGF-140 and can be
corresponds to Tines 39-47 and page
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         0;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Score 52.6; DB 2;
Pred. No. 0.00016;
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                                                                                                                                                                                                               FACTOR
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                                                                                                                                                                                                                                                                                                                                     Matches 140;
                                                                                                                                                                                                                                                                                                                                                      Query Match
Best Local Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         TELEPHONE: (212) 527-7700
TELEPAX: (211) 753-6237
INFORMATION FOR SEQ ID NO: 2:
SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         DESCRIPTION: HYPOTHETICAL:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            REFERENCE/DOCKET NUMBER: 5986/13586-US7 TELECOMMUNICATION INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          FILING DATE: April 4, 19
APPLICATION NUMBER: 07/0
FILING DATE: June 16, 19
ATTORNEY/AGENT INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               CLASSIFICATION: 536
PRIOR APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              COMPUTER: IBM PC compatible OPERATING SYSTEM: PC/MS-DOS SOFTWARE: Wordperfect 5.1 CURRENT APPLICATION DATA:
                                  529
                                                                                                   469
                                                                                                                                                                     409
                                                                                                                                                                                                      134
                                                                                                                                                                                                                                      349
                                                                                                                                                                                                                                                                                             ANTI-SENSE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             MOLECULE TYPE:
 311
                                                                                                                                    194
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APPLICATION NUMBER: 07
APPLICATION NUMBER: 07
                                                                                                                                                                                                                                                                                                                                                                                                                    IDENTIFICATION METHOD:
OTHER INFORMATION: Th
OTHER INFORMATION: fo
                                                                                                                                                                                                                                                                74 GCATCGGCTTCCACCTCCAGGCGCTCCCGACGGCGCGCATCGGCGGCGCGCACGCGGACA 133
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          NAME/KEY:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          STRANDEDNESS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             NAME: Howard M. Frankfort REGISTRATION NUMBER: 32,6
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              APPLICATION NUMBER:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        TYPE: nucleic acid
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         ENGTH:
                                                                                            TCGACCCGGAGAACTGCAGGTTCCAACACCAGACGCTGGAAAAACGGGTACGACGTCTACC
                                                                                                                                                                                                CCCGCGACAGCCTGCTGGAGCTCTCGCCCGTGGAGCGGGCGTGGTGAGCATCTTCGGCG
AGTCCTACAAGTACCCCGGCATGTTCA 337
                                ACTCTCCTCAGTATCACTTCCTGGTCA
                                                               TCACC---GATGAGTGCACGTTCAAGGAGATTCTCCTTCCCAACAACTACAACGCCTACG
                                                                                                                               TGGCCAGCCGGTTCTTCGTGGCCATGAGCAGCAAGGGCAAGCTCTATGGCTCGCCCTTCT
                                                                                                                                                                TGATGAGCAGAAGATACCTCTGCATGGATTTCAGAGGCAACATTTTTGGATCACACTATT
                                                                                                                                                                                                                               CCATCTACAGTGCCCTGATGATCAGATCAGAGGATGCTGGCTTTGTGGTGATTACAGGTG
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UMBER: 07/901,705
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                                                                                                                                                                                                                                                                                                                                                    3.3%;
                                                                                                                                                                                                                                                                                                                                                                                                                  This sequence can be found on page 5, lines 3-13, in the application, as filed.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             08/187,780
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                                                                                                                                                                                                                                                                                                                                   0;
                                                                                                                                                                                                                                                                                                                                Score 52.6; DB 4;
Pred. No. 0.00016;
0; Mismatches 124
                                                                                                                                                                                                                                                                                                                                                                  DB 4;
                                                                                                                                                                                                                                                                                                                                                                  Length 423;
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US-08-478-486F-5 ; Sequence 5, Application US/08478486F ; Patent No. 6432702

RESULT 6

ENERAL INFORMATION

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                                                                                                                                                                                                                                           Query Match
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APPLICATION NUMBER: 07/806,771
FILING DATE: December 6, 1991
APPLICATION NUMBER: 07/177,506
FILING DATE: Appril 4, 1988
APPLICATION NUMBER: 07/062,925
FILING DATE: June 16, 1987
ATTORNEY/AGENT IMPORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   TELEFAX: (212) 753-6237
INFORMATION FOR SEQ ID NO:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     TELEPHONE: (212) 527-7700
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            TYPE: nucling STRANDEDNESS: sing
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                CLASSIFICATION: 536
PRIOR APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC/MS-DOS
SOFTWARE: Wordperfect 5.1
CURRENT APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   COMPUTER READABLE FORM:
MEDIUM TYPE: floppy Diskette,
MEDIUM TYPE: 1.44 MB storage
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         MOLECULE TYPE:
                        409
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    CORRESPONDENCE ADDRESS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       NUMBER OF SEQUENCES:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        TITLE OF INVENTION: MAMMALIAN GROWTH FACTOR
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          APPLICANT: CLAUDIO BASILICO
APPLICANT: DANIELA TALARICO
                                                                                               349
                                                                                                                                                                   289 GGAACAGCTACCACCTGCAGATCCACAAGAATGGCCATGTGGATGGCGCACCCCATCAGA 348
                                                                                                                                   74
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     FILING DATE: January 25, 1994
APPLICATION NUMBER: 07/901,705
FILING DATE: June 22, 1992
APPLICATION NUMBER: 07/806,771
                                                                                                                                                                                                                            Local Similarity
                                                                                                                                                                                                                                                                                                OTHER INFORMATION:
OTHER INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        REGISTRATION NUMBER: 32,613
REFERENCE/DOCKET NUMBER: 5986/13586-US7
                                                                                                                                                                                                                                                                                                                                                       OTHER INFORMATION:
OTHER INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          FILING DATE:
                                                                                                                                                                                                                                                                                                                                                                                            LOCATION:
IDENTIFICATION METHOD:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              NAME: Howard M. Frankfort
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   APPLICATION NUMBER:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       APPLICATION NUMBER: US/08/478,486F
FILING DATE: June 7, 1995
CLASSIFICATION: 536
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             COUNTRY:
                                                                                                                                                                                                                                                                                                                                                                                                                                NAME/KEY:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                      DESCRIPTION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     ADDRESSEE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 ENGTH:
TGATGAGCAGAAGATACCTCTGCATGGATTTCAGAGGCAACATTTTTGGATCACACTATT 468
                                                     CCATCTACAGTGCCCTGATGATCAGATCAGAGGATGCTGGCTTTGTGGTGATTACAGGTG 408
                                                                                                                             GCATCGGCTTCCACCTCCAGGCGCTCCCCGACGGCCGCATCGGCGGCGCGCACGCGGACA 133
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Genomic DNA
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 08/187,780
                                                                                                                                                                                                       0; Mismatches 124;
                                                                                                                                                                                                                        Score 52.6; DB 4;
Pred. No. 0.00016;
                                                                                                                                                                                                                                       Length 423;
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                                                  Query Match
Best Local Similarity
                                       Matches 140;
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                                                                                                                                                                                                                                           INFORMATION FOR SEQ ID NO:
                                                                                                                                TOPOLOGY: 1: MOLECULE TYPE:
                                                                                                                                                                                                                                                                                                                                    ATTORNEY/AGENT INFORMATION:
NAME: Howard M. Frankfort
REGISTRATION NUMBER: 32,6
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         CLASSIFICATION: 536
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 08/187,780
FILING DATE: January 25, 1994
                                                                                                                                                                                                                        SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                             TELECOMMUNICATION INFORMATION: TELEPHONE: (212) 527-7700
                                                                                                                                                                                                                                                                                                                                                                                      APPLICATION NUMBER: 07/806;
FILING DATE: December 6, 199
APPLICATION NUMBER: 07/177;
FILING DATE: April 4, 1988
APPLICATION NUMBER: 07/062;
FILING DATE: June 16, 1987
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                COMPUTER READABLE FORM:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              APPLICANT: CLAUDIO BASILICO
APPLICANT: DANIELA TALARICO
289 GGAACAGCTACCACCTGCAGATCCACAAGAATGGCCATGTGGATGGCGCACCCCATCAGA 348
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           CORRESPONDENCE ADDRESS:
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OPERATING SYSTEM: PC/MS-DO
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    MEDIUM TYPE: Floppy Diskette,
MEDIUM TYPE: 1.44 MB storage
COMPUTER: IBM PC compatible
                                                                                                                                                                STRANDEDNESS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                FILING DATE: January 25, 1994
APPLICATION NUMBER: 07/901,705
FILING DATE: June 22, 1992
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           APPLICATION NUMBER: US/08, FILING DATE: June 7, 1995
                                                                                                                                                                                    TYPE: nucleic acid
                                                                                                                                                                                                                                                              TELEFAX:
                                                                                                                                                                                                                                                                                                                   REFERENCE/DOCKET NUMBER:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    SOFTWARE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                COUNTRY: USA
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                                                                                                                                                 ss: single
linear
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                                                      3.3%;
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                                                      Score 52.6; DB 4;
Pred. No. 0.00018;
                                       Mismatches
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                                                                         DB 4;
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                                                                     Length 528;
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RESULT 8
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APPLICANT: ROGERS, DAVID T.; WOLFMAN, NEIL M.; SEEHRA, JASBIR S.
TITLE OF INVENTION: HOMOGENEOUS K-FGF AND USE OF THE SAME
                                                                                                                                                                                                                                                                                                                                                                        Sequence 9, Application US/08478486F Patent No. 6432702
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Matches 140;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Query Match
Best Local Similarity
                                                                                                                                                                                                                                                                                                                                               GENERAL INFORMATION:
                                                                                                                                                             ADDRESSEE: Darby & D
                                                                                                                                                                                                                                                                                     APPLICANT:
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APPLICATION NUMBER: 438,278
FILING DATE: 16-NOV-1989
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/0
FILING DATE: 12-JUN-1992
                                                                                                                                                                                                                          NUMBER OF SEQUENCES:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      NUMBER OF SEQUENCES:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           302 TGGCCAĞCCĞGTTCTTCGTGGCCATGAGCAGCAAGGGCAAGCTCTATGGCTCGCCCTTCT 361
                                                                                                                                                                                                                                                         PPLICANT: DANIELA
ITLE OF INVENTION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         362 TCACC---GATGAGTGCACGTTCAAGGAGATTCTCCTTCCCAACAACTACAACGCCTACG
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                                                                             STATE:
                                                                                                                                       STREET:
                                                 COUNTRY:
                                                                                                     CITY: New York
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               LENGTH: 599
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        AGTCCTACAAGTACCCCGGCATGTTCA 448
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               ACTOTOCTOAGTATOACTTCCTGGTCA 555
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                                                                                                                                                                                                                                                                                     CLAUDIO BASILICO
DANIELA TALARICO
                                                                                                                                                             & Darby P.C
                                                                                                                                                                                                                                                      MAMMALIAN GROWTH FACTOR
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US-08-478-486F-11
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                                                                                                                                                                                                                                          Sequence 11, Application US/08478486F Patent No. 6432702
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Best Local Similarity
                                                                                                                  GENERAL INFORMATION:
APPLICANT: CLAUDIO BASILICO
APPLICANT: CALADIO BASILICO
APPLICANT: DANIELA TALLARICO
APPLICANT: DANIELA TALLARICO
APPLICANT: DANIELA TALLARICO
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MEDIUM TYPE: Floppy Diskette, 3
MEDIUM TYPE: 1.44 MB storage
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC/MS-DOS
SOFTWARE: Wordporfect 5.1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                INFORMATION FOR SEQ ID NO: SEQUENCE CHARACTERISTICS:
                        NUMBER OF SEQUENCES: 12
CORRESPONDENCE ADDRESS:
ADDRESSEE: Darby & Darby P.C.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                REFERENCE/DOCKET NUMBER: 5986/13586-US7
TELECOMMUNICATION INFORMATION:
TELEPHONE: (212) 527-7700
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            FILING DATE: June 16, 198
ATTORNEY/AGENT INFORMATION:
NAME: Howard M. Frankfort
REGISTRATION NUMBER: 32,6
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           409
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STRANDEDNESS: sing
TOPOLOGY: linear
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APPLICATION NUMBER: 07/177,50
FILING DATE: April 4, 1988
APPLICATION NUMBER: 07/062,92
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     APPLICATION NUMBER: US/08/478,486F FILING DATE: June 7, 1995
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805 Third Avenue
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(212) 753-6237
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Pred. No. 0.00019;
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FILING DATE: December 6, 1991
APPLICATION NUMBER: 07/17,506
FILING DATE: April 4, 1988
APPLICATION NUMBER: 07/062,925
FILING DATE: April 4, 1988
APPLICATION NUMBER: 07/062,925
FILING DATE: June 16, 1987
ATTORNEY/AGENT INFORMATION:
NAME: Howard M. Frankfort
REGISTRATION NUMBER: 32,613
REFERENCE/DOCKET NUMBER: 5986/13586-US7
TELECOMMUNICATION: INFORMATION:
TELEPHONE: (212) 527-7700
TELECAX: (212) 753-6237
INFORMATION FOR SEQ ID NO: 11:
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                                                        Sequence 11, Application PC/TUS9306251
GENERAL INFORMATION:
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Best Local Similarity
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MEDIUM TYPE: Floppy Diskette,
MEDIUM TYPE: 1.44 MB storage
                  APPLICANT: Wickstrom, Eric and Rife, Jason P.
TITLE OF INVENTION: Trivalent Synthesis of Oligonucleotides Containing
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PRIOR APPLICATION DATA:
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FILING DATE: January 25, 1997
APPLICATION NUMBER: 07/901,705
APPLICATION NUMBER: 22, 1992
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                                                                                                                                                                                AGTCCTACAAGTACCCCGGCATGTTCA 777
                                                                                                                                                                                                                                                         TCACC--
                                                                                                                                                                                                                                                                                                                                      TGGCCAGCCGGTTCTTCGTGGCCATGAGCAGCAAGGCAAGCTCTATGGCTCGCCCTTCT
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                                                                                                                                                                                                                   ACTCTCCTCAGTATCACTTCCTGGTCA 555
                                                                                                                                                                                                                                                                                              TCGACCCGGAGAACTGCAGGTTCCAACACCAGACGCTGGAAAAACGGGTACGACGTCTACC 528
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    OF INVENTION:
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June 22, 1992
77,806,771
7991
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Stereospecific Alkylphosphonates and Arylphosphonates
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Pred. No. 0.00027;
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; MOLECULE TYPE: DNA (genomic)
PCT-US93-06251-11
                                  Sequence 1, Application US/07915934
Patent No. 5360893
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Query Match 3.3%; Score 52.6; DB 5; Best Local Similarity 52.4%; Pred. No. 0.00028; Matches 140; Conservative 0; Mismatches 124
                   GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             TELEPHONE: 516-742-43.
TELEFAX: 516-742-4366
TELEX: 230 901 SANS UI
INFORMATION FOR SEQ ID NO:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   REGISTRATION NUMBER: 31,346
REFERENCE/DOCKET NUMBER: 85
TELECOMMUNICATION INFORMATION:
TELEPHONE: 516-742-4343
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            SEQUENCE CHARACTERISTICS:
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 APPLICANT:
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SOFTWARE: Patentin Polaria
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CLASSIFICATION:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             NAME: DiGiglio, Frank
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                                                                                                                                                                                                                                                                                                                                                                                  CCCGCGACAGCCTGCTGGAGCTCTCGCCCGTGGAGCGGGGGCGTGGTGAGCATCTTCGGCG 710
                                                                                                                                                                                                                                                                                                                                                                                                               CCATCTACAGTGCCCTGATGATCAGATCAGAGGATGCTGGCTTTTGTGGTGATTACAGGTG 408
                                                                                                                                                                                          ACTCTCCTCAGTATCACTTCCTGGTCA
                                                                                                                                                                                                                                                                                                        TGGCCAGCCGGTTCTTCGTGGCCATGAGCAGCAAGGGCAAGCTCTATGGCTCGCCCTTCT 770
                                                                                                                                                                                                                                                                                                                                         TGATGAGCAGAAGATACCTCTGCATGGATTTCAGAGGCAACATTTTTTGGATCACACTATT 468
                                                                                                                                                                                                                               TCACC---GATGAGTGCACGTTCAAGGAGATTCTCCTTCCCAACAACTACAACGCCTACG
                                                                                                                                                                                                                                                                 TCGACCCGGAGAACTGCAGGTTCCAACACCAGACGCTGGAAAAACGGGTACGACGTCTACC
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        1219 base pairs
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OWENS, GREGORY P.
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NUMBER OF SEQUENCES: 4

CORRESPONDENCE ADDRESS:
ADDRESSEE: FREDERICK W. PEPPER, PH.D.

STREET: 11545 W. BERNARDO COURT, STE. 302

TITLE OF INVENTION: DNA SEQUENCES ENCODING PROTEINS USED TO TITLE OF INVENTION: ELICIT AND DETECT PROGRAMMED CELL DEATH

APPLICANT:

COHEN, J. J. HAHN, WILLIAM E.

SAN DIEGO

USA

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US-08-325-743-1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                       RESULT 13
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Best Local Similarity 67.0%;
                                                                                                                                                                                                                                                                                                                                                                                                              Sequence 1, Application US/08325743
Patent No. 5527682
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 TELEFAX: (619) 451-9628
INFORMATION FOR SEQ ID NO:
SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                                                                                                                              ENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            1238
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          1178 GAGAAGGGGTCTCTCCCAACATATTTCTCTTCCTTGTGCCTCTCCTCTTTATCACTTTTA 1237
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
COMPUTER: PATEN: PC-DOS/MS-DOS
SOFTWARE: PATENTIN Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION UMBER: US/08/325,743
FILING DATE: 19-OCT-1994
CLASSIFICATION: 435
CLASSIFICATION: 435
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC Compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
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                                                                                                                                                                                                                                                                 ORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                                                                                       TITLE OF INVENTION:
                                                                                                                                                                                                                                                                                                                                                                                 PPLICANT:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       ATTORNEY/AGENT INFORMATION:
NAME: PEPPER PH.D., FREDERICK W.
REGISTRATION NUMBER: 31,286
REFERENCE/DOCKET NUMBER: 92-0224
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         NAME/KEY:
LOCATION:
                                                                                                                                                                                               STREET: 11545 W
CITY: SAN DIEGO
STATE: CA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           LENGTH: 972 base pairs
TYPE: NUCLEIC ACID
STRANDEDNESS: single
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             APPLICATION NUMBER: US/07/915,934 FILING DATE: 19920720 CLASSIFICATION: 435
                                                                                                                                                                              COUNTRY:
                                                                                                                                                                                                                                                  ADDRESSEE:
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                                                                                                                                                                                                                                   11545 W.
                                                                                                                                                                              USA
                                                                                                                                                                                                                                                                                                                                      OWENS, GREGORY P. COHEN, J. J. HAHN, WILLIAM E.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          DNA (genomic)
                                                                                                                                                                                                                                                                                                    DNA SEQUENCES ENCODING PROTEINS USED TO ELICIT AND DETECT PROGRAMMED CELL DEATH
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 0; Mismatches
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              DB 1;
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US-09-240-952-1
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Best Local Similarity
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NFORMATION FOR SEQ ID NO:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        TELEFAX: (619) 451-9628 INFORMATION FOR SEQ ID NO: SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 1238 AGCATAAAAAAAAAAAAAAAAAAAAAAAAAAAAA 1274
                                                                                                                                                                                                                                           COMPUTER READABLE FORM:

MEDIUM TYPE: 3.5 inch, 1.44 Mb i
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
                              TELEPHONE: 650/225-1489
                                                                                                      FILING DATE: 12-Mar-98
ATTORNEY/AGENT INFORMATION:
                                                                                                                                                                                                                SOFTWARE: WinPatin (Ge
CURRENT APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                                                       NUMBER OF SEQUENCES: 5
CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                     APPLICANT:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    REFERENCE/DOCKET NUMBER: 31,286
REFERENCE/DOCKET NUMBER: 92
TELECOMMUNICATION INFORMATION:
                                                                                                                                                     PRIOR APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                                                                                       TITLE OF INVENTION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  FEATURE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     APPLICATION NUMBER: US 0: FILING DATE: 20-JUL-1992 ATTORNEY/AGENT INFORMATION: NAME: PEPPER PH.D., FREDI
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             MOLECULE TYPE: DNA (genomic)
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LOCATION:
                                                         NAME: Svoboda, Craig G.
REGISTRATION NUMBER: 39,044
REFERENCE/DOCKET NUMBER: P1
                                                                                                                                                                                                                                          COMPUTER: IBM PC
OPERATING SYSTEM:
                 TELEFAX:
                                                                                                                                                                   FILING DATE: 2
CLASSIFICATION:
                            TELEPHONE:
                                                                                                                                                                                                  APPLICATION NUMBER:
                                                                                                                                                                                                                                                                                                                          COUNTRY:
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                                                                                                                                     APPLICATION NUMBER:
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: California
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              650/952-9881
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La Fleur, Mon:
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                                                                                                                                                                                                                                                                                                                                                                                       Genentech, Inc.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   2.8%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                    Method of Preventing the Death of Retinal
                                                                                                                                                                                                                                                                                                                                                                                                                                    Neurons and Treating Ocular Diseases
                                                                                                                                                                                                                              (Genentech)
                                                                                                                                      09/041,383
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                                                                                                                                                                                              US/09/240,952
                                                                                                                                                                                                                                                                          1.44 Mb floppy disk
                                                            P1088P1
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; Sequence 167, Application US/09484970B
; Patent No. 6426186
; GENERAL INFORMATION:
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SEQ ID NO 167
LENGTH: 1234
TYPE: DNA
ORGANISM: Homo mapiens
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                                                                                                                                                                                                                                                                                                                                                                                                                                        ; FEATURE:
; NAME/KEY: misc feature
; OTHER INFORMATION: Incyte ID No. 6426186 333034.1
US-09-484-970B-167
                                                                                                                                                                                                                                                                                                                                                                       Query Match 2.8%;
Best Local Similarity 50.0%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Best Local Similarity Matches 141; Conserv
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Best Local :
                                                                                                                                                                                                                                                                                                                                                     Matches 141;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          CURRENT APPLICATION NUMBER: US/09/484,970B
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   NUMBER OF SEQ ID NOS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      APPLICANT: Volkmuth, Wayne
APPLICANT: Walker, Michael G.
TITLE OF INVENTION: BONE REMODELING GENES
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         FILE REFERENCE:
      679
                                                                                                                                                                              559
                                                                                                                                                                                                                 311 CCACAAGAATGGCCATGTGGATGGCGCACCCCATCAGACCATCTACAGTGCCCTGATGAT 370
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        251 CTGGGGTGGCCTGATCCACCTGTACACAGCCACAGCCAGGAACAGCTACCACCTGCAGAT 310
                                        431 CATGGATTTCAGAGGCAACATTTTTGGATCACACTATTTCGACCCGGAGAACTGCAGGTT 490
                                                                                                                             371 CAGATCAGAGGATGCTGGCTTTGTGGTGATTACAGGTGTGATGAGCAGAAGATACCTCTG 430
                                                                                                                                                                                                                                                                                                251 CTGGGGTGGCCTGATCCACCTGTACACAGCCACAGCCAGGAACAGCTACCACCTGCAGAT 310
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                451 CAGGGAGCGTTTTCAAGAAAATAGCTATAATACCTATGCCTC 492
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   394 GATGTCAAAAAAGGAAAACTCCATGCAAGTGCCAAGTTCA---CAGATGACTGCAAGTT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        334 ATTTGCTGTGTCTCAGGGGATTGTAGGAATACGAGGAGTTTTCAGCAACAAATTTTTAGC 393
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 274
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            311
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   TYPE: Nucleic Acid
STRANDEDNESS: Single
                                                                                                                                                                     CTACCCGGATGGCAAAGTCAATGGATCCCACGAAGCCCAATATGTTAAGTGTTTTGGAAAT 618
GATGTCAAAAAAAGGAAAACTCCATGCAAGTGCCAAGTTCA---CAGATGACTGCAAGTT
                                                                                                                                                                                                                                                              CTCGGGGCGCCGGACCGGCAGCCTCTACTGCAGAGTGGGCATCGGTTTCCATCTGCAGAT 558
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         CCAACACCAGACGCTGGAAAACGGGTACGACGTCTACCACTC 532
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             CATGGATTTCAGAGGCAACATTTTTGGATCACACTATTTCGACCCGGAGAACTGCAGGTT 490
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                                                                                    ATTTGCTGTGTCTCAGGGATTGTAGGAATACGAGGAGTTTTCAGCAACAATTTTTAGC 678
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Jones, Karen A.
                                                                                                                                                                                                                                                                                                                                                     Conservative
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                                                                                                                                                                                                                                                                                                                                                                       Score 45.2; DB 4; Length 1234; Pred. No. 0.025;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Mismatches 138;
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Search completed: May 29, 2003, 00:07:03 Job time : 82 secs

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Maximum Match 100%
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Maximum DB seq length: 2000000000
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Gapop 10.0 , Gapext 1.0
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1612
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Pred. No. is the number of results predicted by chance to have

score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result 234.: 234.: 230. 528 457.4 448.8 428 Score Query Match 99 204909 178533 204909 290471 Length 170200 76884 1869 2137 2137 2137 2137 2137 2137 2137 B AX351022 AX275042 BC018404 AX249747 AX250100 AX097639 AX481448 AB018122 BC017664 AX076891 AX092981 AX403730 AX454492 AX454492 AF263537 AB047858 AX191707 AC008012 AX403623 AX464132 AB021975 AX149492 AC125991 AX191715 AC130862 AC015538 AX358824 AX156434 AX481451 AX156436 AF110400 AX362317 AX191713 AC130862 AX235431 AX481467 AX249749 AB025716 AB037973 AX403623 Sequence AX464132 Seminary AC103292 Rattus no AC130862 Rattus no AC015538 Mus muscu AC130862 Rattus no AC125991 Rattus no AX191715 Sequence AX097639 Sequence AX097639 Sequence AX454492 AX490970 AX275042 Sequence BC018404 Homo sapi AF263537 Homo sapi AB047858 Homo sapi AX191707 Sequence AX249747 Sequence AX250100 Sequence AB037889 Mus muscu AX191709 Sequence AF263536 Mus muscu AB078777 Rattus no AX351022 AB021975 AB037973 Homo sapi AX464132 Sequence AX249749 Sequence Description AB025718 Mus 2 Sequence 7 Sequence Sequence Sequence Sequence Sequence Sequence Sequence Homo sapi Homo sapi Sequence Sequence Sequence Sequence Homo sapi Homo sapi Sequence

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ALIGNMENTS

TITLE	AUTHORS	REFERENCE			ORGANISM	SOURCE	KEYWORDS	VERSION	ACCESSION	DEFINITION	LOCUS	AF263537	RESULT 1
Lorenz-Deplereux, B., Grabowski, M., Meitinger, T. and Strom, T.M. Autosomal dominant hypophosphataemic rickets is associated with	White, K.B., Evans, W.E., O'Riordan, J.L.H., Speer, M.C., Econs, M.J.,	1 (bases 1 to 1612)	Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.	Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;	Homo sapiens	Homo sapiens.	•	AF263537.1 GI:9964291	AF263537	Homo sapiens FGF23 (FGF23) mRNA, complete cds.	AF263537 1612 bp mRNA linear PRI 14-DEC-2000		

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Best Local Similarity
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541 ATCACTTCCTGGTCAGTCTGGGCCGGGCGAAGAGAGCCTTCCTGCCAGGCATGAACCCAC
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                                                                                                                                                                                                                               GATACCTCTGCATGGATTTCAGAGGCAACATTTTTGGATCACACTATTTCGACCCGGAGA
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Muenchen 80336, Germany
Location/Qualifiers
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Nat. Genet. 26 (3), 345-348 (2000)
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/db_xref="G1:9964292"
/db_xref="G1:9964292"
/translation="MLGARIRLWVCALCSVCSMSVLRAYPNASPLLGSSWGGLIHLYT
ATTARNSYHLQIHKNGHVDGAPHQTIYSALMIRSEDAGFVVITGVMSRRYLCMDFRGNI
FGSHYPDPENCRROHQTLENGYDVYHSPQYHFLVSLGRAKRAFLPGMNPPPYSQFLSR
RNEIPLIHFNTPIPRRHTRSAEDDSERDPLMVLKPRARMTPAPASCSQELPSAEDNSP
MASDPLGVYRGGRVMTHAGGTGPEGCRPFAKFI"
MASDPLGVYRGGRVMTHAGGTGPEGCRPFAKFI"

MASDPLGVYRGGRVMTHAGGTGPEGCRPFAKFI"
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/map="12p13.3"
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|db_xref="taxon:9606"
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ATCATAATAGAAAACTCAGCCTCCCTACAGGGTGAGCACCTTCTGTCTCG 	IGGTGGTAGGCTGGTGAAAACTTGACAGCTAGACTTGATGCTTGCAA 	aCACTACTTTCAAGCCTTCGTTCTTCCTTGAGCATCTCTGGGGAAGAGC 	CACTGGCATTTGAGTGTGCABACCTTGACATTAACAGCTGAATGGGGCA 	ATTOGGAGATCCCAGAAGCTTCTCCACTGCCCTATGCATTTATGTTAGA 	261 AAAAAAAAAAAAGCAGTGGGTTCCTGAGCTCAAGACTTTGAAGGTGTAGGGAAGAGGA 13: 	TITCTCTTCCTTGTGCCTCTCCTCTTTATCACTTTTAAGCATAAAAAA 	acaggtaaactagaaatttccccttcatgaaggtagagagaagggtct 	CATGGGGTTTCACCGCCTTCCTCACTCCATATAGAACACCTTTCCCAAT 	TGCTTCTCTGGGGTCCCTTCCACAGGAGGTCCTGTGAGAACCAACC	GACCAGGTCCCTTGACGTTCCGAGGATGGGAAAGGTGACAGGGGCATGT 	AGGGTCGCTGGAAGGGCACCCTCTTAACCCATCCCTCAGCAAACGCAG 	TGAACACGCACGCTGGGGGAACGGCCCGGAAGGCTGCCGCCCCTTCGC 	GCGCCGAGGACAACAGCCCGATGGCCAGTGACCCATTAGGGGTGGTCAG 	TGCTGAAGCCCGGGCCCGGATGACCCCGGCCCCGGCCTCCTGTTCACA 	CCATACCACGGCGGCACACCCGGAGCGCCGAGGACGACTCGGAGCGGGA	CCCCGTACTCCCAGTTCCTGTCCCGGAGGAACGAGATCCCCCTAATTCA	
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GAGCAGGACGATGTTTGGGGGCCCCCCTCAGGCTCTGGGTCTGTGCCTTGTTGCAGGGTCT	99.1%; Score 1598; DB 9; 100.0%; Pred. No. 0; Vative 0; Mismatches 0; ATCCTCACACCAGCTACTTGCAAGGGAGAA 3ATCCTCACACCAGCTACTTGCAAGGGAGAA	/gene="hypf" /note="a candidate for the responsible gene for ADHR" /codon start=1 /product="tumor-derived hypophophatemia inducing factor" /product="tumor-derived hypophophatemia inducing factor" /protein_id="BAB5589]." /db_xref="GI:14196227" /translation="MLGARLRLMYCALCSVCSMSVLRAYPNASPLIGSSWGGLIHLYT /translation="MLGARLRLMYCALCSVCSMSVLRAYPNASPLIGSSWGGLIHLYT ATARNSYHLQIHKNGHVDGAPHQTIYSALMIRSEDAGTVVITGYMSERYLCMDFRGNI FGSHYFDDENCRFGHQTLENGYDVYHSPQYHFIVSLGRAKRAFLFGMNPPFYSQFLSR RMEIPLHHRNTPIPRRHTRSAEDDSERDPLNVLKPRARMTPAPASCSQELPSAEDNSP MASDPLGVVRGGRVNTHAGGTGPEGCRPFAKFI" MASDPLGVVRGGRVNTHAGGTGPEGCRPFAKFI" MASDPLGVVRGGRVNTHAGGTGPEGCRPFAKFI"	1. 3004 /organism="Homo sapiens" /db xref="taxon:9606" 1. 3004 /gene="hypf" 133. 888	Takeyoshi Yamashita, search Lab., Miyahara tyamashita@kirin.co.j	1 (Bites) 2 (Bites) 2 (Bites) 2 (Bites) 2 (Bites) 2 (Bites) 3 (Bites) 3 (Bites) 3 (Bites) 4 (Bites) 4 (Bites) 5 (Bites) 5 (Bites) 6 (Bit	3004 is hypf mRNA for tu plete cds. GI:14196226 is cDNA to mRNA. is Metazoa, Chordata,
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Mammalla; Eutheria; Primates;
1 (bases 1 to 1211)
Conklin, D.C.
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Patent: WO 0149740-A 1 12-JUL-2001;
ZymoGenetics, Inc. (US)
Location/Qualifiers
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RNEIPLIHFMTPIFRAHTFRSAEDDSERDPLNYLKFPRARMTPAPASCSQELPSAEDNSP
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Homo sapiens.
Homo sapiens
Eukaryota; Metazoa;
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BAC RPCI11-388F6
complete sequence
 Chordata;
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 Craniata;
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 Vertebrata;
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Cancer Institute
 Euteleostomi;
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REFERENCE AUTHORS REFERENCE AUTHORS TITLE JOURNAL REFERENCE AUTHORS REFERENCE AUTHORS REFERENCE REFERENCE AUTHORS TITLE TITLE JOURNAL JOURNAL AUTHORS JOURNAL JOURNAL TITLE JOURNAL Submitted (15-MAR-2002) Human Genome Sequencing Center, Depart of Molecular and Human Genetics, Baylor College of Medicine, Baylor Plaza, Houston, TX 77030, USA On Aug 24, 1999 this sequence version replaced gi:5708398.

INFORMATION: http://www.hgsc.bcm.tmc.edu/ or email Muzny,D., Arenson,A.D., Bouck,J., Bunac,C., Chen,Z., Ding,Y.,
Dugan,S., Durbin,J., Forcum,J., Garcia,C., Gorrell,J.L.,
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Zhou,X., Kucherlapati,R., Nelson,D. and Gibbs,R.A. Submitted (28-SEP-2001) Human Genome Sequencing Center, Department of Molecular and Human Genetics, Baylor College of Medicine, One Baylor Plaza, Houston, TX 77030, USA Submitted (09-OCT-1999) Human Genome Sequencing Center, Department of Molecular and Human Genetics, Baylor College of Medicine, One Baylor Plaza, Houston, TX 77030, USA of Molecular and Human Baylor Plaza, Houston, 4 (bases 1 to 170200) Submitted (10-JUL-1999) Human Genome Sequencing Center, Department of Molecular and Human Genetics, Baylor College of Medicine, One Baylor Plaza, Houston, TX 77030, USA 3 (bases 1 to 170200) of Molecular and Human Baylor Plaza, Houston, 6 (bases 1 to 170200) Worley, K.C. Direct Submission Worley, K.C. Direct Submission Worley, K.C. Direct Submission Direct Submission Worley, K.C. Submitted Direct Submission Worley, K.C. Unpublished Direct Submission Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo. 1 (bases 1 to 170200) (bases 1 to 170200) (bases 1 to 170200) (24-AUG-1999) Human Genome Sequencing Center, Department lar and Human Genetics, Baylor College of Medicine, One aza, Houston, TX 77030, USA Department

CLONE LENGTH: This sequence does not necessarily represent the entire insert of this clone. Overlapping regions of clones are o sequenced and submitted once, so the sequence for the remainder the insert may be found in the record for the adjacent clones. Overlapping clones are noted at the beginning and end of the Overlapping clones are noted at the beginning Features listing. only r of

COMMENT

gc-help@bcm.tmc.edu

ANNOTATION OF FEATURES:

STSs are identified using ePCR (Genome Res. 7:541-550) searches of a local database that includes entries from dbSTS, GDB, and local mapping efforts.

Repeats are identified using RepeatMasker (A. Smit and P. Green, unpublished.) for Human and Mouse sequences.

Genes and Region of sequence similarity are identified by BLAST (Nuc. Acids Res. 25:3389-3402) similarity (expect < 1e-34) to the EST and cDNA sequences. Genes demonstrate at least two exons flanked by consensus splice sites that maintained sequence continuity across the splice junctions. Sequences that are not identical matches are annotated as similar.

standard of double strand coverage with a minimum of 2 clones and 2 reads with no ambiguities or 2 chemistries with a minimum of 2 clones and 3 reads with no ambiguities. If the sequence quality for a region does not meet this standard, it will be indicated in the SEQUENCING READ COVERAGE: Sequencing is completed to a minimum Low Coverage.

QUALITY OF INDIVIDUAL BASES: This sequence meets stringent quality standards - estimated error rate less than 1 per 10,000 bases. Reports of lowest quality individual bases and measures of base quality are listed below. Description of the metrics can be found at VRL: http://gc.bcm.tmc.edu:8088/quality.info/genbank.annotation

QUALSTAT-REPORT----

Summary Statistics

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Distribution of Quality < 40

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FEA

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RESULT 5 AX403623 LOCUS DEFINITION ACCESSION VERSION VERSION KEYWORDS SOURCE ORGANISM REFERENCE AUTHORS	1542 134724 1602 134784	Qy 1362 <i>i</i> Db 134544 <i>i</i> Qy 1422 <i>i</i> Db 134604 <i>i</i> Qy 1482 Qy 1482 Qy 1482 Qb 134664 Q	Qy 1182 J Db 134364 J Qy 1242 7 Db 134424 7 Qy 1302 Qy 1302 Qy 1304444 0	Qy 1002 (Db 134184 (Qy 1062 (Db 134244 (Qy 1122 ; Db 134304 7	Qy 822 (Db 134004 (Qy 882 (Db 134064 (Qy 942) Db 134124)
AX403623 AX403623 Sequence 510 from Patent WO0073454. AX403623 AX403623 AX403623.1 GI:21437088 human. Homo sapiens Bukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Bukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Ammmalia; Eutheria; Primates; Catarrhini; Hominidae; Homo. 1 Ashkenazi,A.J., Baker,K.P., Botstein,D., Desnoyers,L., Eaton,D., Perrara,N., Gerber,H., Gerritsen,M., Goddard,A., Godowski,P., Grimaldi,C.J., Gurney,A.L., Kljavin,I., Napier,M.A., Pan,J.,	AGGGTGAGCACCT 1601 AGGGTGAGCACCT 13478	ATGTTAGATGCCCCGATCCCACTGGCATTTGAGTGTGCAAACCTTGACAGTTAACAGCTTGA 1421	AGGGGTCTCTCCCAACATATTTCTCTTCCTTGTGCCTCTCTTTTATCACTTTTAAGCA 1241	GGGCATGTATGGAATTTGCTGCTCTCTGGGGTCCCTTCCACAGGAGGTCCTGTGAGAAC 1061	TIGGTCAGGGGCGGTCGAAGTGAACACGCACGCTGGGGAACGGGCCCGGAAAGGCTGCCGC 881

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CTGAACGTGCTGAAGCCCCGGGCCCGGATGACCCCCGGCCCCCGGCCTCCTGTTCACAGGAG
                                       AACACCCCCATACCACGGCGGCACACCCCGGAGGGCCGAGGACCGACTCGGAGCGGGGACCCC
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Eukaryota; Metazoa; Chordata; Craniata; Vertebrata;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae;
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Genentech Inc. (US)
Location/Qualifiers
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Pred. No. 1e-181;
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                                        GAAAACGGGTACGACGTCTACCACTCTCCTCAGTATCACTTCCTGGTCAGTCTGGGCCGG
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Sequence 3
AX249749
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Patent: WO 0166596-A 3 13-SEP-2001;
CHIRON CORPORATION (US) ; Kyoto University (JP
Location/Qualifiers
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/db_xref="taxon:9606"
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RESULT 8
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1 (baees 1 to 756)

Itoh,N. and Kavanaugh,M.W.
Human fgf-23 gene and gene expression products
Patent: WO 0166595-A 3 13-SEP-2001;
CHIRON CORPORATION (US); Kyoto University (JP)
Location/Qualifiers
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Ribopharma AG (DE)
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Mammalia; Eutheria;
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Direct Submission
Submitted (03-FEB-2000) Nobuyuki Itoh, Kyoto University, Graduat School of Pharmaceutical Sciences, Department of Genetic Biochemistry; Yoshida-Shimoadachi, Sakyo, Kyoto, Kyoto 606-8501, Japan (E-mail:itohnobu@pharm.kyoto-u.ac.jp, Tel:81-75-753-4540, Fax:81-75-753-4600)
                                                                                                                                                                                                                                                       Biochem. Biophys. Res.
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/db_xref="taxon:9606"
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/db_xref="GI:15593932"
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Pred. No. 7.2e-171;
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Sequence 3 from Patent W00149740.
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Patent: WO 0149740-A 3 12-JUL-2001;
ZymoGenetics, Inc. (US)
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1 (bases 1 to 753)
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White, K.E., Evans, W.E., O'Riordan, J.L.H., Speer, M.C., Econs, M.J., Lorenz-Depiereux, B., Grabowski, M., Meitinger, T. and Strom, T.M. Autosomal dominant hypophosphataemic rickets is associated with
                                                                                                                                                                                                                                                                                                                                                                                                                                                       Submitted (03-MAY-2000) Medizinische Muenchen 80336, Germany
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Strom, T.M.
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/product="rGF23"
/protein_id="AGG09916.1"
/brotein_id="AGG09916.1"
/db_xref="GI:9964290"
/translation="MLGTCLRLLVGVLCTVCSLGTARAYPDTSPLLGSNWGSLTHLYT
/translation="MLGTCIRLLVGVLCTVCSLGTARAYPDTSPLLGSNWGSLTHLYT
/TATTSYHLQIRGDTHQTTFHQTTYSLALMITSSDAGRSVVITGARAKRIFQPGTNPPPFSQFLAR
RGSLHFSPENGKKFRQMTLENGYDVYLSQKHYLVSLGRAKRIFQPGTNPPPFSQFLAR
RNEVPLLHFYTVRPRHHTRSAEDPPERDPLNVLKPRPRATPVPVSCSRELPSAEEGGP
AASDDLGVLRRGGDARGGAGGADRCRPFPRFV"
                                                                                                                                                                                                                                                                    /gene="Fgf23"
57. .812
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/db_xref="taxon:10090"
/chromosome="6"
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Pred. No. 1.8e-99;
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Direct Submission

Submitted (24-JAN-2002) Nobuyuki Itoh, Kyoto University Graduate Submitted (24-JAN-2002) Nobuyuki Itoh, Kyoto University Graduate School of Pharmaceutical Sciences, Department of Genetic Blochemistry; Yoshida-Shimoadachi, Sakyo, Kyoto 606-8501, Japan (B-mail:itohnobuspharm.kyoto-u.ac.jp, Tel:81-75-753-4540, Fax:81-75-753-4600)
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ASDPLGVLRRGRGDARRGAGTDRORPFPRFY"

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/codon_start=1
/product="fibroblast growth
/protein_id="BAB84108.1"
/db_xref="GI:18376671"
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|. .756
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Pred. No. 1.9e-97;
0; Mismatches 192
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Db.	601 CCCA	CCCATACCGGTATCCTGCTCGCGAGAGCTACCGAGTGCAGAGGAAGGTGGCCCCGCGGCC 660
Ş	807 AGTG	AGTGACCCATTAGGGGTGGTCAGGGGCGGTCGAGTGAACACGCACG
D	661 AGCGA	AGCGACCCCTGGGAGTGCTGCGCAGAGGCCGCGGGGATGCTCGCCGGGGCGCGGGAAGGC 720
ş	867 CCGGI	CGGAAGGCTGCCGCCCTTCGCCAAGTTCATCTAG 902
용	721 ACGGI	ACGEATCGGTCTCCCCTTTCCCAGGTTCGTCTAG 756
RESUI AX249	T 15	
DEFIN	LOCUS AXX	AX249747 756 bp DNA linear PAT 28-SEP-2001 Sequence 1 from Patent WO0166596.
VERSION KEYWORDS		149747.1 GI:15864368
SOURCE	NISM	
REFER	RENCE 1	zukaryota; metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus. l (bases l to 756)
TIT	AUTHORS Itc	h, N. and Kavanaugh, M. W. ian fgf-23 gene and gene expression products
FEATURES	į.	PACENC: WO 0166596-A 1 13-SEP-2001; CHIRON CORPORATION (US) ; Kyoto University (JP) Location/Qualifiers
	Bource	1756 /organism="Mus musculus" /db wref="tayon-10000"
BASE ORIGI	COUNT	141 a 251 c 217 g 147 t
Que Bes Mat	Query Match Best Local Si Matches 551;	tch 26.6%; Score 428; DB 6; Length 756; al Similarity 72.9%; Pred. No. 2e-92; S51; Conservative 0; Mismatches 205; Indels .0; Gaps 0;
д V	147 ATGTT 1 ATGCT	ATGITEGGGGCCCCCCCCAGGCTCTGGGTCTGTGCCTTGTGCAGCGTCTGCAGCATGAGC 206
Ş	207 GTCCT	GTCCTCAGAGCCTATCCCAATGCCTCCCCACTGCTCGGCTCCAGCTGGGGTGGCCTGATC 266
g	61 ACTGC	TAGAGCCTATCCAGACACTTCCCCATTGCTTGGCTCCAACTCGGGGAAGCCTGACC 120
음 중	267 CACCT	ACCTGTACACAGCCACAGCCAGGAACAGCTACCACCTGCAGATCCACAAGAATGGCCAT 326
5 5		GTGGATGGCGCACCCCATCAGACCATCTACAGTGCCCTGATGATCAGATCAGATCAGAGGATGCT 386
, 5		IGGUACCCCCATCAGACCATCTACAGTGCCCTGATGATTACATCAGAGGACGCC 240
유 성	387 GGCTT 241 GGCTC	GGCTTTGTGGTGATTACAGGTGTGATGAGCAGAAGATACCTCTGCATGGATTTCAGAGGC 446
Ş	447 AACAT	TTTTGGATCACACTATTTCGACCCGGAGAACTGCAGGTTCCAACACCCAGACGCTG 506
9	301 AACAT	AACATTTTTGGATCGCTTCACTTCAGCCCAGAGAATTGCAAGTTCCGCCAGTGGACGCTG 360
유 장	507 GAAAA 361 GAGAA	GARARCGGGTRCGRCGTCTRCCACTCTCCTCRGTATCRCTTCCTGGTCRGTCTGGGCCGG 566
음 성	567 GCGAA 421 GCCAA	GCGAAGAGAGCCTTCCTGCCAGGCATGAACCCACCCCCGTACTCCCAGTTCCTGTCCCGG 626
; &		AGGAACGAGATCCCCCTAATTCACTTCAACACCCCCATACCACGGGGGCACACCCGGAGC 686
5	481 AGGAA	CGAGGTCCCGCTGCTGCACTTCTACACTGTTCGCCCACGCGCGCACACGCGCAGC 540

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721	867	661	807	601	747	541	687
721 GCGGATAGGTGTCGCCCCTTTCCCCAGGTTCGTCTAG 756	867 CCGGAAGGCTGCCGCCCTTCGCCAAGTTCATCTAG 902	AGCGATCTTCTGGGGGTGCTGCGCAGAGGCCCTGGAGATGCTCGCGGGGGGGCGCGGGAGCC 720	807 AGTGACCCATTAGGGGTGGTCAGGGGCGGTCGAGTGAACACGCACG	601 CCTGTGCCTGTATCCTGCTCTCGCGAGCTGCCGAGCGCAGAGGAAGGTGGCCCCGCAGCC 660	747 CCGGCCCCGGCCTCCTGTTCACAGGAGCTCCCGAGCGACCCGAGGACAACAGCCCGATGGCC 806	541 GCCGAGGACCCACCGAGCGCGACCCACTGAACGTGCTCAAGCCGGGGCCCCGCGCCACG 600	687 GCCGAGGACCACTCGGAGCGGGACCCCCTGAACGTGCTGAAGCCCCGGGCCCCGGATGACC 746

Search completed: May 29, 2003, 01:28:07 Job time: 4859 secs

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Result
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Maximum Match 100%
Listing first 45 s
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Maximum DB seq length: 200000000
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Title:
                                                                                                                                                                                                                                                                                                 Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.
                              194.5
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2: sp_bacteria:*
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sp_rodent:*
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3 Q42407
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                                                                  Q8vi81 rattus norv
Q9erw3 rattus norv
Q8vcy9 mus musculu
Q95k97 macaca fasc
O9ygd8 oncorhynchu
O8r4x0 rattus norv
O42407 gallus gall
O8gg59 ambystoma m
Q9dfc9 brachydanio
                                                                                                                      Q8vi82 rattus norv
Q8vi80 rattus norv
Q9dn0 gallus gall
Q8r519 rattus norv
Q9yh31 notophthalm
Q90xq5 ambystoma m
Q90xq1 ambystoma m
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121 ENGYDVYHSPQYHFLVSLGRAKRAFLPGMNPPPYSQFLSRRNEIPLIHFNTPIPRRHTRS 180	61 VDGTPHQTIYSALMITSEDAGSVVIIGAMTRRFLCMDLRGNIFGSYHFSPENCRFRQWTL 120	61 VDGAPHQTIYSALMIRSEDAGFVVITGVMSRRYLCMDFRGNIFGSHYFDDENCRFQHQTL 120	1	1 MLGARLRLWCALCSVCSWSVLRAYPNASPLLGSSWGGLIHLYTATARNSYHLOIHKNGH 60	Query Match 71.9%; Score 978; DB 11; Length 251; Best Local Similarity 71.7%; Pred. No. 3.9e-86; Matches 180; Conservative 26; Mismatches 45; Indels 0; Gaps 0;	SEQUENCE 251 AA; 27911 MW; 35A229E1B3900593 CRC64;	M00442; FGF; 1.	ProDom; PD000831; HB/F_growthfact; 1.	Pfam; PF00167; FGF; 1.	InterPro: IPR002209; HB/F growthfact.		Submitted (JAN-2002) to the EMBL/GenBank/DDBJ databases.	"Rattus norvegicus fgf23.":		SEQUENCE FROM N.A.	(P) =		Rodentia; Sciuroqnathi; Muridae;	Eukaryota: Metazoa: Chordata: Craniata: Vertebrata: Euteleostomi:	Rattus norvegicus (Rat).		growth factor 23.	(TrEMBLrel. 21, Last	(TrEMBLrel. 20,	-2002 (TrEMBLrel.		Q8VI82 PRELIMINARY; PRT; 251 AA.	LT 1

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Best Local S
Matches 67
           NCBI_TaxID=9031;
                                                                                                       Gallus gallus (Chicken).
Eukaryota; Metazoa; Chordata;
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ProDom; PD000831; HB/F growthfact; 1.
SMART; SM00442; FGF; 1.
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Submitted (JAN-2002) to the EMBL/GenBank/DDBJ
EMBL; AB078901; BAB84299.1; -
InterPro; IPR002209; HB/F growthfact.
InterPro; IPR002348; IL1 HBGF.
Pfam; PF00167; FGF; 1.
                                                                                                                                                                                                                                                       01-MAR-2001
01-JUN-2002
                                                                         Archosauria; Aves;
                                                                                                                                                                                                                  Fibroblast growth
                                                                                                                                                                                                                                                                                                                             01-MAR-2001
                                                                                                                                                                                                                                                                                                                                                                      Q9DDNO;
                                                                                                                                                                                                                                                                                                                                                                                                   Q9DDN0
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     01-MAR-2002 (TrEMBLrel. 20, Created)
01-WAR-2002 (TrEMBLrel. 20, Last sequence update)
01-JUN-2002 (TrEMBLrel. 21, Last annotation update)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              SEQUENCE
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          NCBI_TaxID=10116;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     182
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           VGTAHRSPESILELKALKPGVIQILGVKASRFLCQQPDGTLYGSPHFDPEACSFREILLK 130
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             DGAPHQTIYSALMIRSEDAGFVVITGVMSRRYLCMDFRGNIFGSHYFDPENCRFQHQTLE 121
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       LWVCLLLPVFLLGVCEAYPISDSSPLL--QFGGQVRQRYLYTDDDQDTEAHLBIREDGTV
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                TPIPRRHTRSAEDDSERDPLNVLKPRARMTPAPAS
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      TDRCRPFPRFV 251
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                                                                                                                                                                                                              (Tremblrel. 16, C
(Tremblrel. 16, I
2 (Tremblrel. 21, I
growth factor 19.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       208 AA;
                                                                                                                                                                                                                                                                                                                                                                                                   PRELIMINARY;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Conservative
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             - PDVGSSDPLSMVEPLQGRSPSYAS
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                                                                      Neognathae;
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                                                                                                                                                                                                                                                Created)
Last sequence update)
Last annotation updat
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Score 239;
Pred. No. 4
                                                              Craniata; Vertebrata; Euteleostomi;
; Galliformes; Phasianidae; Phasianinae;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Craniata; Vertebrata; Euteleostomi;
Sciurognathi; Muridae; Murinae; Rattus.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   No. 4.5e-15;
smatches 73;
                                                                                                                                                                                                                                                                                                                                                                                                227
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RESULT 4
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Best Local S
Matches 62
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Query Match
Best Local :
                                                                                                                                                                          Submitted (PEB-2002) to the EMBL/GenBank/DDBJ databases EMBL; AB079262; BAB84564.1; -. SEQUENCE 245 AA; 27150 MW; C9305D307E7D0648 CRC64;
                                                                                                                                                                                                                                                            Mammalia; Eutheria;
NCBI_TaxID=10116;
                                                                                                                                                                                                                                                                                      Eukaryota;
                                                                                                                                                                                                                                                                                                                                        01-JUN-2002
01-JUN-2002
                                                                                                                                                                                                                                                                                                                                                                              Q8R5L9
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     PRINTS; PR00262; IIIHBGF.
ProDom; PD000831; HB/F growthfact; 1.
SMART; SM0442; FGF; 1.
PROSITE; PS00247; HBGF FGF; UNKNOWN 1.
PROSITE; PS00247; HBGF FGF; WKNOWN 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         [1]
SEQUENCE FROM N.A.
MEDLINE=20564778; PubMed=11110663;
MEDLINE=2054778; PubMed=11110663;
MEDLINE=2054778; PubMed=11110663;
                                                                                                                                                                                                                                      SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                  Rattus norvegicus (Rat)
                                                                                                                                                                                                                                                                                                                             01-JUN-2002
                                                                                                                                                                                                                                                                                                                                                                Q8R5L9;
  153
                         105
                                                 102
                                                                                                                                                                                                              "Rattus norvegicus FGF3 mRNA.";
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  InterPro; IPR002209; HB/F growthfact.
InterPro; IPR002348; IL1_HBGF.
Pfam; PF00167; FGF; 1.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          HSSP; P09038; 1BFG.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        "Identification of Synergistic Signals
                                                                                                                                                                                                                                                                                                                                                                                                                                          188
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                                                                     LYCAT---KYHLQLHESGRYNGSLENSAYSILEITAVEVGYVAIKGLESGRYLANNKRGR 104
                                                                                             LYTATARNSYHLQIHKNGHVDGAPHQTIYSALMIRSEDAGFVVITGVMSRRYLCMDFRGN 101
 -PYSQFLSRRNEIPLIHFNTPIPR----
                          LYASEHYNAE-
                                              IFGSHYFDPENCRFQHQTLENGYDVYHSPQYHFLVSLGRAKRAFLPGMNPP-----
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                                                                                                                                                                                                                                                                                                                                                                                                                                      GDYSQAFEPEVYSSPLETDS-MDPFGI---TSKLSPVKSPSFQK
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              QHQTLENGYDVYHSPQYHFLVSLGRAK-RAFLPGMNPPPYSQFLSRRNEIPL-----
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     GGDGRVDAVGSQSPQSLLEIRAVAVRTVAIKGVQSSRYLCMDEAGRLHGQLSYSIEDCSF
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            HKNGHVDGAPHQTIYSALMIRSEDAGFVVITGVMSRRYLCMDFRGNIFGSHYFDFENCRF 115
                                                                                                                                                                                                                                                                                                                                                                                                                                                               -IHFNTPIPRRHTRSAEDDSERDPLNVLKPRARMTPAPASCSQE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         1 Similarity 67; Conserv
                                                                                                                                     Similarity
                                                                                                                                                                                                                                                                                       Metazoa;
                                                                                                                                                                                                                                                                                                                         (TrEMBLrel. 21, (TrEMBLrel. 21, (TrEMBLrel. 21,
                                                                                                                           Conservative
                                                                                                                                                                                                                                                                                                                                                                             PRELIMINARY;
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                                                                                                                                                                         AA;
                        CEFVERIHELGYNTYASRLYRTGPSGPGARRQ-
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                                                                                                                                                                                                                                                                         Chordata;
Rodentia;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   14.3%;
                                                                                                                                   13.3%; Score 181.5;
29.0%; Pred. No. 1.
                                                                                                                        29;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        30;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Score 194.5;
Pred. No. 9.7e
30; Mismatches
                                                                                                                                                                                                                                                                                                                         Last sequence up
                                                                                                                                                                                                                                                                                                                                                   Created)
                                                                                                                                                                                                                                                                         Craniata; Vertebrata; Euteleostomi; Sciurognathi; Muridae; Murinae; Rat
                                                                                                                                                                                                                                                                                                                                                                           PRT;
                                                                                                                                                                       C9305D307E7D0648 CRC64;
                                                                                                                         Mismatches
-RHTRSAEDDSERDPLNVLKPRARMTPAPA
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                                                                                                                                     1.9e-09;
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                                                                                                                         , 98
                                                                                                                                              11;
                       -PGAQRPWYVSVNGKG
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 204
                                               152
                       161
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RESULT OF YEAR OF THE PROPERTY OF THE PROPERTY
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Best Local S
Matches 39
                                                                                                                                                                                                                                                                    Q90XQ5;
Q1-DEC-2001 (TrEMBLrel. 19, Created)
Q1-DEC-2001 (TrEMBLrel. 19, Last sequer
Q1-UUN-2002 (TrEMBLrel. 21, Last annot;
Fibroblast growth factor 4 (Fragment).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           PROSITE; PS00225; CRYSTALLIN BETAGAMMA; UNKNOWN_1.

PROSITE; PS00247; HBGF FGF; 1.

PROSITE; PS00247; HBGF FGF; 1.

PROSITE; PS00247; HBGF FGF; AC4688CD989C6EAF CR
       MEDLINE=21439472; PubMed=11555861; Christensen R.N., Weinstein M., Tassava R.A.; "Fibroblast growth factors in regenerating limbs of and semi-quantitative RT-PCR expression studies."; J. Exp. Zool. 290:529-540(2001).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Putative fibroblast growth factor-4.
Notophthalmus viridescens (Eastern newt) (Triturus viridescens).
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Amphibia; Batrachia; Caudata; Salamandroidea; Salamandridae;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       HSSP;
  EMBL;
                                                                                                                                                                                                                                                      Eukaryota; Metazoa;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         PRINTS; PR00262; IL1HBGF.
ProDom; PD000831; HB/F_growthfact;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         InterPro; IPR002348; I
Pfam; PF00167; FGF; 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  "Putative Newt Fibroblast Submitted (OCT-1996) to the
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             1 EHX 60
                                                                                                                                   SEQUENCE FROM N.A.
                                                                                                                                                                         NCBI_TaxID=8296;
                                                                                                                                                                                                           Ambystoma
                                                                                                                                                                                                                              Amphibia; Batrachia;
                                                                                                                                                                                                                                                                                                                                                                                                                    Q90XQ5
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AF360984;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       U76998; AAC98812.1; P09038; 1BFF.
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                                                                                                                                                                                                                                                                                                                                                                                                                  PRELIMINARY;
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                                                                                                                                                                                                                                               Chordata;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           11.6%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        нв/F growthfact.
IL1_HBGF.
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HB/F_growth
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21,
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                                                                                                                                                                                                                                                                                                                Created)
Last sequence upo
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Score 158; DB
Pred. No. 2.6e
16; Mismatches
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                                                                                                                                                                                                                     Craniata; Vertebrata; Euteleostomi; Salamandroidea; Ambystomatidae;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   AC4688CD989C6EAF CRC64;
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                                                              Ambystoma:
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                                                           Cloning
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Best Local (
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Best Local (
Q8VI81;
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01-MAR-2002
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01-JUN-2002
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NON TER
SEQUENCE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       EMBL;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Ambystoma maculatum (spotted salamander).
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Amphibia; Batrachia; Caudata; Salamandroidea; Ambystomatidae;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             01-DEC-2001 (TrEMMBLrel. 19, Created)
01-DEC-2001 (TrEMBLrel. 19, Last sequence of the control o
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PROSITE; PS00225; CRYSTALLIN BETAGAMMA; 
PROSITE; PS00247; HBGF_FGF; UNKNOWN 1.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             MEDLINE=21439472; PubMed=11555861;
Christensen R.N., Weinstein M., Tassava R.I
"Fibroblast growth factors in regenerating
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Pfam; PF00167; FGF;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Ambystoma
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     semi-quantitative RT-PCR expression Exp. Zool. 290:529-540(2001). L; AF360988; AAL16961.1; -.
                                                                                                                                                                                       BECKFKEPLLANNYNAYESROYPGMYIALSKNGRTKR
                                                                                                                                                                                                                                                                                                              YHLQIHKNGHVDGAPHQTIYSALMIRSEDAGFVVITGVMSRRYLCMDFRGNIFGSHYFDP 110
                                                                                                                                                                                                                                ENCREQUETLENGYDVYHSPQYH----FLVSLGRAKR
                                                                                                                                                                                                                                                                       FHVOVLPDGKIHGTHNENRYSLLEISPVERGVVSILGVKSALFLAMNNRGKLYGSKQYS-
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                                                                                                                                                                                                                                                                                                                                                                                 Similarity
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                                                                                                                                                                                                                                                                                                                                                                                                                                           111
111 AA;
                                                                                    PRELIMINARY;
                                                                                                                                                                                                                                                                                                                                                           Conservative
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36.1%;
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Pred. No. 1.9e
18; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Last annotation
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Pred.
                                                                                    PRT;
                                                                                                                                                                                                                                                                                                                                                                                                                                             4A3A52ED39001057 CRC64;
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No. 6.8e-07;
                                                                                  218
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cing limbs
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20, 20, 21,

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01-MAR-2001
01-JUN-2002
                                                        PRINTS; PRO0262; ILHHBGF.
ProDom; PD000831; HB/F growthfact;
SMART; SM00442; FGF; 1
PROSITE; PS00247; HBGF FGF; 1
PROSITE; PS00247; HBGF FGF; 1
SEQUENCE 192 AA; 21604 MW; 7734
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         PRINTS; PR00262; IL1HBGF.

ProDom; PD000831; HB/F growthfact; 1.

SMART; SM00442; FGF; 1-

PROSITE; PS00247; HBGF FGF; UNKNOWN 1.

SEQUENCE 218 AA; 25207 MW; ED898684B5307C58 CRC64;
                                                                                                                                                                                                                                                                                                                                                                    SEQUENCE FROM N.A.

TISSUE=DORSAL ROOT GANGLION;

Xiao H., Huang O., Zhang F., Guo C., Chen Z., I

"Rattus norvegicus fibroblast growth factor 13.

Submitted (MAY-2000) to the EMBL/GenBank/DDBJ c

EMBL; AF271786; AAG15492.1;

HSSP; P31371; 1G82.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       "Rattus norvegicus FGF15."; Submitted (JAN-2002) to the EMBL/Geni EMBL; AB078900; BABB4298.1; -. InterPro; IPR002209; HB/F_growthfact InterPro; IPR002348; IL1_HBGF. Pfam; PF00167; FGF; 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Eukaryota; Metazoa;
Mammalia; Eutheria;
NCBI_TaxID=10116;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Q9ERW3;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Q9ERW3
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Fibroblast growth
                                                                                                                                                                                                                                                          InterPro; IPR002209; HB/F_growthfact.
InterPro; IPR002348; IL1_HBGF.
Pfam; PF00167; FGF; 1.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Rattus norvegicus (Rat)
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        KDVSSVRYLCMSADGKIYGLIRYSEEDCTFREEMDCLGYNQYRSMKHHLHIIFIKAKPRE 159
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1 (TrEMBLrel. 16, )
2 (TrEMBLrel. 21, )
growth factor 13.
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Rodentia;
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       10.8%;
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5; Mismatches
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Score 147.5;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Craniata; Vertebrata; Euteleostomi; Sciurognathi; Muridae; Murinae; Rattus.
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                                                                        7736A3671677B263 CRC64;
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annotation update)
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   ВB
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Q8VCY9;
Q1-MAR-2002 (TrEMBLrel. 20, Created)
O1-MAR-2002 (TrEMBLrel. 20, Last sequence update)
O1-JUN-2002 (TrEMBLrel. 21, Last annotation updat
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      SMART; SM00442; FGF; 1.

PROSITE; PS00247; HBGF_FGF; UNKNOWN 1.
SEQUENCE 245 AA; 27587 MW; 5B96D41
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ProDom; PD000831; HB/F growthfact;
SMART; SM00442; FGF; 1.
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Submitted (DEC-2001) to the EMBL/GenBank/DDBJ databases
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InterPro; IPR002348; IL1_HBGF.
Pfam; PF00167; FGF; 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                TISSUE=RETINA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      NCBI_TaxID=10090;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Eukaryota; Metazoa;
Mammalia; Eutheria;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    FGF13.
Mus musculus (Mouse)
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211
                                                   215
                                                                                                                                                       156
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               156 QFLSRRNEIPLIHFNTPIPRRHTRSAEDDSERDPLNVLKPRARMTPAPASCSQ-ELPSAE
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                                                                                                                                                                                                                                                                                                              68
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   72
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                                                                                                                                                                                                                                                                                                                                                            3.7 GGLIHLYTATARNSYHLQIHKNGHVDGAPHQ-TIYSALMIRSEDAGFVVITGVMSRRYLC
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DITEFSRSGSGTPTKSRSVSGVLNGGKSMSHNEST
                                                                                                                                                 QFLSRRNEIPLIHFNTPIPRRHTRSAEDDSERDPLNVLKPRARMTPAPASCSQ-ELPSAE
                                                                                                                                                                                                                                                     MDFRGNIFGSHYFDPENCRFQHQTLENGYDVYHSPQYHFLVSLGRAKRAFLPGMNPPPYS
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                MNSEGYLYTSEHFTPE-CKFKESVFENYYVTYSSMIYR----QQQSGRGWYLGLN----
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 MDFRGNIFGSHYFDPENCRFQHQTLENGYDVYHSPQYHFLVSLGRAKRAFLPGMNPPPYS
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                                                                                                                                                                                                     MNSEGYLYTSEHFTPE-CKFKESVFENYYVTYSSMIYR----QQQSGRGWYLGLN-----
                                                                                                                                                                                                                                                                                                                                                                                                                     54;
                                                                                                                                                                                                                                                                                                                                                                                                                                             Similarity
                                                                                                      -KEGEJ
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                                                NSPMASDPL-GVVRGGRVNTHAGGT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             factor 13.
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                                                                                                                                                                                                                                                                                                                                                                                                                                             10.8%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              HB/F
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  -MKGNHVKKN----
                                                                                                                                                                                                                                                                                                                                                                                                                  31;
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                                                                                                                                                                                                                                                                                                                                                                                                                  Score 147.5; Core 147.5; Score 147.5; Core 147.5; Core Pred. No. 3.6e
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1; Mismatches 81;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Craniata; Vertebrata; Euteleostomi; Sciurognathi; Muridae; Murinae; Mus
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           5B96D41AC3A3DF78 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                  .6e-06;
les 81;
                                                239
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           192
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         239
                                                                                                   -KPAAHFLPKPLKVAMYKEPSLH
                                                                                                                                                                                                                                                                                                                                                                                                                                                                     DB 11;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            -KPAAHFLPKPLKVAMYKEPSLH 157
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Length
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RESULT 11 Q95K97 ID Q95K9

Q95K97

PRELIMINARY;

PRT;

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RESULT
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Rotinopterygii; Neopterygii; Teleostei; Euteleostei; Protacanthopterygii; Salmoniformes; Salmonidae; Oncori NCBI TaxID=8022;
                                                 InterPro; IPR001064; Crystallin.
InterPro; IPR002209; HB/F growth
InterPro; IPR002348; IL1_HBGF.
Pfam; PF00167; PGF; 1.
PRINTS; PR00262; IL1HBGF.
                                                                                                                                                                                                                                                                       mammalian vertebrate: Continuous expressi fiber hyperplasia.", Biochim. Biophys. Acta 1443:305-314(1998) EMBL; Y16850; CAA766422.1; -. HSSP; P31371; 1G82.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     SEQUENCE FROM N.A.
MEDLINE=99096461; PubMed=9878802;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               01-MAY-1999 (TrEMBLrel. 10, Created)
01-MAY-1999 (TrEMBLrel. 10, Last sequence update)
01-JUN-2002 (TrEMBLrel. 21, Last annotation update)
PERSONAL PROPERTY OF THE PROPERTY O
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01-DEC-2001
01-DEC-2001
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01-DEC-2001 (TrEMBLrel. 19, Last sequence update)
01-JDC-2002 (TrEMBLrel. 21, Last annotation update)
11-JUN-2002 (TrEMBLrel. 21, Last annotation update)
12-JUN-2002 (TrEMBLrel. 21, Last annotation update)
13-JUN-2002 (TrEMBLrel. 21, Last annotation update)
14-JUN-2002 (TrEMBLrel. 21, Last annotation update)
15-JUN-2002 (TrEMBLrel. 21, Last annotation update)
16-JUN-2002 (TrEMBLrel. 21, Last annotation update)
17-JUN-2002 (TrEMBLrel. 21, Last sequence update)
18-JUN-2002 (TrEMBLrel. 19, Last sequence upd
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            "Identification of a fibroblast
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Osada N., Hida M., Kusuda J., Tanuma R., Iseki
Suzuki Y., Sugano S., Hashimoto K.;
"Isolation of full-length cDNA clones from mac
libraries.";
Submitted (JUN-2001) to the EMBL/GenBank/DDBJ
EMBL; AB063051; BAB60779.1;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         PRODOM; PD000831; HB/F growthfact; 1.
PROSITE; PS00247; HBGF FGF; UNKNOWN 1.
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PD000831; HB/F_growthfact;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 205
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208 AA; 2
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IL1_HBGF.
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Pred. No. 3.7e
20; Mismatches
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                                        Fibroblast growth factor Gallus gallus (Chicken). Eukaryota; Metazoa; Chor Archosauria; Aves; Neogn
                         Archosauria;
Gallus.
                                                                                                                                                                                 042407;
01-JAN-1998
                                                                                                                                    01-JUN-1998
01-JUN-2002
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Liu C., Dib-Hajj S.D., Waxman S.G.;
Liu C., Dib-Hajj S.D., Waxman S.G.;
"Fibroblast growth factor homologous factor-4D.";
Submitted (FEB-2001) to the EMBL/GenBank/DDBJ dat.
EMBL, AF348523; AAL83904.1; -.
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01-JUN-2002 (TrEMBLrel. 21, Last sequence update)
01-JUN-2002 (TrEMBLrel. 21, Last annotation update)
01-JUN-2002 (TrEMBLrel. 21, Last annotation update)
NCBI_TaxID=9031;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Eukaryota; Metazoa; Chordata;
Mammalia; Eutheria; Rodentia;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         SMART; SM00442; FGF; 1.
PROSITE; PS00225; CRYST
PROSITE; PS00247; HBGF
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PS00247; HBGF FGF; 1.
206 AA; 23375 MW; BB883328F17EB6E4 CF
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B (TrEMBLrel. 06,
2 (TrEMBLrel. 21,
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                                          Neognathae;
                                                                      Chordata;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                23346 MW;
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24.7%;
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                                          Craniata; Ver; ; Galliformes;
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                                          Vertebrata; Euteleostomi;
mes; Phasianidae; Phasiani
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78;
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Best Local Similarity
Matches 38; Conserv
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               SEQUENCE FROM N.A.

MEDLINB=21826199; PubMed=11836784;

Christensen R.N., Weinstein M., Tassava R.A.;

"Expression of fibroblast growth factors 4, 8, and 10 in limbs,
flanks, and blastemas of ambystoma.";

Lev. Dyn. 223:193-203(2002).

EMBL; AY034453; AAK59700.1; -.

SEQUENCE 201 AA; 22994 MW; 89EA1E61806A6F57 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Q8QG59;
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SEQUENCE FROM N.A.
MEDLINE=97330690; PubMed=9187149;
Ohuchi H., Nakagawa T., Yamamoto A., Araga A., Ohta T.,
Yoshioka H., Kuwana T., Nohno T., Yamasaki M., Itoh N.,
"The mesenchymal factor, FGF10, initiates and maintains
of the chick limb bud through interaction with FGF8, an
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               InterPro; IPR002209; HB/F_growthfact.
Pfam; PF00167; FGF; 1.
ProDom; PD000831; HB/F_growthfact; 1.
SMART; SM00442; FGF; 1.
SEQUENCE 212 AA; 23631 MW; AB4C0B32C72A0D90 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        01-JUN-2002 (TrEMBLrel. 21, Created)
01-JUN-2002 (TrEMBLrel. 21, Last sequence update)
01-JUN-2002 (TrEMBLrel. 21, Last annotation update)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Ambystoma mexicanum (Axolotl).
Eukaryota; Metazoa; Chordata;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Fibroblast growth factor 10
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            EMBL; D86333; BAA24945.1;
HSSP; P31371; 1G82.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             NCBI_TaxID=8296;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 108 FDPENCRFQHQTLENGYDVY-----HSPQYHFLVSLGR--AKRA-----FLP 147
140 KLKERMEENKYNTYASYKWRH--
                                                           114 RFQHQTLENGYDVYHSPQYHFLVSLGRAKRAF--LPGMNPPPYSQFLSRRN 162
                                                                                                                                                                                           55
                                                                                                                                                                                                                                                                                                                                                                                   Local Similarity
nes 47; Conserv
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                                                                                                                         81 IDADGKVSGTTKVDCPYSVMEITSVDVGIVAVKGVYSNYYLAMNEKGRVYGSREFTTD-C
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                                                                                                                                                                                                                                                                                                          6 LRLWYCALCSVC----SWSVLRAYENASPLLG-----SSWGGLIHLYTATARNSYHLQ 54
                                                                                                                                                                                    IHKNGHVDGAPH-QTIYSALMIRSEDAGFVVITGVMSRRYLCMDFRGNIFGSHYFDPENC 113
                                                                                                                                                                                                                                                   LLLWVSCLSVTCHDLARDMLSPEVANSSVPVVGRQVRSYKHLEGDVRLRRLLCVTNYFLK 80
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                                                                                                                                                                                                                                                                                                                                                                            10.5%; Score 143; DB 13; 27.5%; Pred. No. 7.6e-06; tive 25; Mismatches 79;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            19; Mismatches
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Pred. No. 7.3e-06;
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-KOROMÉVALNGKGTÉKRGOKTKŔKN 185
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                                                                                                                                                                                                                                                                                                                                                                                   79;
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, Noji S.;
s the outgrowth
n apical
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Search completed: May 23, 2003, 07:45:45 Job time : 86 secs

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Result
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1 MLGARLRLWVCALCSVCSMS......VNTHAGGTGPEGCRPFAKFI 251
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FGF5 KOUSE
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FGF3 CHICK
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4 homo sapien
1 gallus gall
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128 9.4 194 1 FGF7 MOUSE 127 9.3 194 1 FGF7 SHEEP 127 9.3 194 1 FGF7 SHEEP 127 9.3 194 1 FGF7 HUMAN 126 9.3 194 1 FGF7 HUMAN 124.5 9.2 162 1 FGFM MOUSE 118.5 8.7 170 1 FGFM HUMAN 118 8.7 208 1 FGF9 MOUSE 118.8 8.7 208 1 FGF9 MOUSE 118.8 7 208 1 FGF9 MOUSE 118.7 208 1 FGF9 MOUSE	9.4 194 1 9.3 194 1 9.3 194 1 9.3 194 1 9.3 162 1 8.7 208 1 8.7 208 1 8.7 208 1 8.7 208 1 8.6 154 1	45	44	4.3	42	41	40	39	38	37	36	35	34
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		FGF2_MOUSE	FGF2_RAT	FGF9_RAT	FGF9_MOUSE	FGF9_HUMAN	FGFM_HUMAN	FGFM_MOUSE	FGF7_HUMAN	FGFC_HUMAN	FGF7_SHEEP	FGF7_PIG	FGF7_MOUSE

ALIGNMENTS

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ROT entry is copyright. It is produced through a collab Swiss Institute of Bioinformatics and the EMBL outst Bioinformatics Institute. There are no restrictions profit institutions as long as its content is in this statement is not removed. Usage by and for communities a license agreement (See http://www.isb-sib.ch/anmail to license@isb-sib.ch).	SEQUENCE FROM N.A. PubMed=11344269; Shimada T., Mizutani S., Muto T., Yoneya T., Hino R., Takeda S., Takeuchi Y., Fujita T., Fukumoto S., Yamashita T.; "Cloning and characterization of FGF23 as a causative factor of tumor-induced osteomalacia."; Proc. Natl. Acad. Sci. U.S.A. 98:6500-6505(2001). -!- SUBCELLULAR LOCATION: Secreted (Potential). -!- DISBASE: DEFECTS IN FGF23 ARE THE CAUSE OF AUTOSOMAL DOMINANT HYPOPHOSEPHATMANIC RICKETS (ADHR). ADHR IS CHARACTERIZED BY LOW SERUM PHOSPHORUS CONCENTRATIONS, RICKETS, OSTEOMALACIA, LEG DEFORMITIES, SHORT STATURE, BONE PAIN AND DENTAL ABSCESSES. -!- SIMILARITY: BELONGS TO THE HEPARIN-BINDING GROWTH FACTORS FAMILY.	SEQUENCE FROM N.A. SEQUENCE FROM N.A. MEDLINE=20490027; PubMed=11032749; Yamashita T., Yoshioka M., Itoh N.; "Identification of a novel fibroblast growth factor, FGF-23, preferentially expressed in the ventrolateral thalamic nucleus of the brain."; Biochem. Biophys. Res. Commun. 277:494-498(2000). [2] SEQUENCE FROM N.A., VARIANTS ADHR Q-176; Q-179 AND W-179, AND VARIANTS M-239. WHITE K.E., Evans W.E., O'Riordan J.L.H., Speer M.C., Econs M.J., Lorenz-Deplereux B., Grabowski M., Meitinger T., Strom T.M.; "Autosomal dominant hypophosphataemic rickets is associated with mutations in FGF23."; Mat. Genet. 26:345-348(2000).	

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16-OCT-2001
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                                               SEQUENCE FROM N.A.
MEDLINE-20490027; PubMed=11032749;
Yamashita T., Yoshioka M., Itoh N.;
"Identification of a novel fibroblast
                              preferentially expressed
brain.";
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SIGNAL
SEQUENCE
                                                                                                         Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus
                                                                                                                                  Mus musculus
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InterPro; IPR002348; IL1 HBGF.
Pfam; PF00167; FGF; 1.
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MIM; 193100;
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HSSP; P03968;
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m; PD00831; HB/F growthfac
F; SM00442; FGF; FALS
ITE; PS00247; HBGF FGF; FALS
th factor; Signal; Disease m
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                   Biophys. Res.
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factor-23 precursor (FGF-
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R -> W (IN ADHR).
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Pred. No. 4e-116;
Mismatches (
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FIBROBLAST GROWTH
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/FTId=VAR_010718.
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Best Local S
Matches 177
                                                                        FGFL MOUSE
Q9JJN1;
16-OCT-2001
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                                                                                                             MOUSE
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SIGNAL
                                    Fibroblast
                                                 16-OCT-2001
16-OCT-2001
                          FGF21.
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MGD; MGI:1891427; F9f23.
InterPro; IPR002209; HB/F growthfact.
InterPro; IPR002348; IL1_HBGF.
Pfam; PF00167; FGF; 1.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           MEDLINB=20517346; PubMed=11062477;
White K.E., Evans W.E., O'rRordan J.L.H., Speer M.C., Econs Lorenz-Deplereux B., Grabowski M., Medinger T., Strom T.M.;
"Autosomal dominant hypophosphataemic rickets is associated
            Mus musculus
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Growth factor; Signal.
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ProDom; PD000831; HB/F_growthfact;
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SUBCELULAR LOCATION: Secreted (Potential).
TISSUE SPECIFICITY: MAINLY EXPRESSED IN THE BRAIN; PREFERENTIALLY EXPRESSED
LOW LEVELS. IN BRAIN; PREFERENTIALLY EXPRESSED
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177; Conserv
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 Metazoa;
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(Rel. 40, Last annotation (FGF-
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27757
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Pred. No. 5.7e
25; Mismatches
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FIBROBLAST
Craniata; Vertebrata;
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                                                                                                210
                                    update)
(FGF-21)
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                                                                                                                                                                                                                                                                                                                                                                                                                     5.7e-80;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                       GROWTH
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                       FACTOR-23.
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                                                                                                                                                                                                          GVLRRGRGDARGGAGG
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cions on its
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RA Arakawa T., Hara A., Fukunishi Y., Konno H., Adachi J., Fukuda S.,
RA Aizawa K., Izawa M., Nishi K., Kiyosawa H., Kondo S., Yamanaka I.,
RA Saito T., Okazaki Y., Gojobori T., Bono H., Kasukawa T., Saito R.,
RA Saito T., Okazaki Y., Gojobori T., Bono H., Kasukawa T., Saito R.,
RA Kadota K., Matsuda H.A., Ashburner M., Batalov S., Casavant T.,
RA Kuehl P., Lewis S., Matsuo Y., Nikaido I., Pesole G., Quackenbush J.,
RA Schriml L.M., Staubli F., Suzuki R., Tomita M., Wagner L., Washio T.,
RA Sakai K., Okido T., Furuno M., Aono H., Baldarelli R., Barsh G.,
RA Blake J., Boffelli D., Bojunga N., Carninci P., de Bonaldo M.F.,
RA Brownstein M.J., Bult C., Fletcher C., Fujita M., Gariboldi M.,
RA Gustincich S., Hill D., Hofmann M., Hume D.A., Kamiya M., Lee N. H.,
RA Lyons P., Marchionni L., Mashima J., Mazzarelli J., Mombaerts P.,
RA Nordone P., Ring B., Ringwald M., Rodriguez I., Sakamoto N.,
RA Sasaki H., Sato K., Schoenbach C., Seya T., Shibata Y., Storch K.-F.,
RA Mynshaw-Boris A., Yoshida K., Hasegawa Y., Kawaji H., Kohtsuki S.,
                                                                                                                                            Query Match
Best Local S
Matches 71
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       HSSP; P03968; IBAR.
MGD; MGI:1861377; Fgf21.
InterPro; IPR002209; HB/F growthfact.
Pfam; PF00167; FGF; 1.
Pfam; PF00167; FGF; 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              the European Bioinformatics Institute. There are no restrictions on its use by non-profit institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial entities requires a license agreement (See http://www.isb-sib.ch/announce/
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Wynshaw-Boris A.,
Hayashizaki Y.;
                                                                                                                                                                                                               SEQUENCE
                                                                                                                                                                                                                                                                                              PRINTS; PR00262; IL1HBGF.
ProDom; PD000831; HB/F_growthfact;
SMART; SM00442; FGF; 1.
                                                                                                                                                                                                                                                                                  PROSITE;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        or send
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     MEDLINE=20461777; PubMed=10858549;
Nishimura T., Nakatake Y., Konishi M., Itoh N.;
"Identification of a novel FGF, FGF-21, preferentially expressed
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        STRAIN=C57BL/6J; TISSUE=Pancreas; MEDLINE=21085660; PubMed=11217851;
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NCBI_TaxID=10090;
          69
                               60 HVDGAPHQTIYSALMIRSEDAGFVVITGVMSRRYLCMDFRGNIFGSHYFDPENCRFQHQT 115
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                                                                                                    LRLWVCALCSVCSMSVLRAY -- PNASPLLGSSWGGLI ---HLYTATARNS-YHLQIHKNG
                                                                  LGLWVRLLLAVFLLGVYQAYPIPDSSPLL--QFGGQVRQRYLYTDDDQDTEAHLEIREDG 68
                                                                                                                                                                                                                                                         ; PS00247; HBGF_FGF; FALSE_NEG.
                                                                                                                                                              Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       an email to license@isb-sib.ch).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Biophys. Acta 1492:203-206(2000).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Eutheria;
                                                                                                                                                                                                             210 AA;
                                                                                                                                            Conservative
                                                                                                                                                                                                                               29
                                                                                                                                                                                                                                                                                                                                                                                                                                    BAA99416.1; -.
BAB25115.1; -.
LLELKALKPGVIQILGVKASRFLCQQPDGALYGSPHFDPEACSFRELL 128
                                                                                                                                                                                                           210 F
23237 MW;
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                                                                                                                                                            32.3%;
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                                                                                                                                                                          17.7%;
                                                                                                                                          38;
                                                                                                                                                        Score 241; DB 1;
Pred. No. 7.9e-15;
                                                                                                                                                                                                          FIBROBLAST GROWTH FACTOR-21
; AE02AABA6477E6F0 CRC64;
                                                                                                                                                                                                                                             POTENTIAL
                                                                                                                                         Mismatches
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                                                                                                                                                                      Length 210
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RESULT 4
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SEQUENCE
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ProDom; PD000831; HB/F growthfact; 1.

SMART; SM00442; FGF; 1-

PROSITE; PS00247; HBGF FGF; FALSE_NEG.

Growth factor; Signal.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBL outstation the European Bioinformatics Institute. There are no restrictions on its use by non-profit institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial entities requires a license agreement (See http://www.isb-sib.ch/announce/or send an email to license@isb-sib.ch).
                                                                                                                                                                                                                                                                                                  SIGNAL
                                                                                                                                                                                                                                                                                                                                                                                                                                     Genew; HGNC:3678; FGF21
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Biochim. Biophys.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            the liver
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         SEQUENCE FROM N.A.
MEDLINE=20461777; PubMed=10858549;
Nishimura T., Nakateake Y., Konishi M.,
"Identification of a novel FGF, FGF-21,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Homo sapiens (Human).
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          16-OCT-2001 (Rel. 40, Last sequence update)
16-OCT-2001 (Rel. 40, Last annotation update)
Fibroblast growth factor-21 precursor (FGF-21).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Q9NSA1;
16-OCT-2001
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                                                                                                                                                                                                                                                                                                                                                                                       InterPro; IPR002209; HB/F growthfact.
InterPro; IPR002348; IL1_HBGF.
Pfam; PP00167; FGF; 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         16-OCT-2001 (Rel. 40, 16-OCT-2001 (Rel. 40, 16-OCT-2001 (Rel. 40,
                              130
                                                           122
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165 PLIHFNTPIPRRHTRSAEDDSERDPLNVLKPRARMTPAPAS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               179
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                                                                                        70
                                                                                                                     62
                                                                                                                                                  13
                                                                                                                                                                        8 LWYCALCSVCSMSVLRAY---PNASPLIGSSWGGLI----HLYTATARNS-YHLQIHKNGHV
                                                          NGYDVYHSPQYHFLVSL--
                                                                                                              DGAPHQTIYSALMIRSEDAGFVVITGVMSRRYLCMDFRGNIFGSHYFDPENCRFQHQTLE 121
                                                                                                                                            LWVSVLAGLL-LGACQAHPIPDSSPLL--QFGGQVRQRYLYTDDAQQTEAHLEIREDGTV
                             DGYNVYQSEAHGLPLHLPGNKSPHRDPAPRGPARFLPLPGLPPALPEPP
                                                                                  GGAADQSPESILQLKALKPGVIQILGVKTSRFLCQRPDGALYGSLHFDPEACSFRELLLE
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                  AB021975; BAA99415.1;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      LEDGYNVYQS-EAHGLPLRLPQKDSPNQDATSWGPVRFLPMPGLLHEPQDQ
                                                                                                                                                                                                             68;
                                                                                                                                                                                                                          Similarity
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209 AA;
                                                                                                                                                                                                             Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                     1BAR.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               . Acta 1492:203-206(2000).
LOCATION: Secreted (Potential).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             ----PDVGSSDPLSMVEPLQGRSPSYAS
                                                                                                                                                                                                                                                                    209 F
22300 MW;
                                                                                                                                                                                                                          16.4%;
                                                                                                                                                                                                          36;
                                                                                                                                                                                                       Score 222.5; DB 1;
Pred. No. 3.7e-13;
6; Mismatches 70;
                                                                                                                                                                                                                                                                    FIBROBLAST GROWTH FACTOR-21; 27925C52A0023823 CRC64;
                                                                                                                                                                                                                                                                                                 POTENTIAL
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    --VSLGRAKRAFLPGMNPPPYSQFLSRRNEIP 165
                                                       GRAKRAFLPGMNP----PPYSQFLSRRNEI 164
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     209
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                                                                                                                                                                                                       Gaps
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RESULT 5
                                                                                 SOTTE SERVICE 
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           the European Bioinformatics Institute. Thuse by non-profit institutions as long
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             MEDLINB=99132028; PubMed=9931477; Nishimura T., Utsunomiya Y., Hoshikawa M., "Structure and expression of a novel human the fetal brain.";
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Homo sapiens (Human)
Eukaryota; Metazoa; Chordata;
Mammalia; Eutheria; Primates;
                                                                                 SEQUENCE
                                                                                                                          SIGNAL
                                                                                                                                    PROSITE; PS00247; HBGF_FGF; 1. Growth factor; Signal.
                                                                                                                                                                                 SMART;
                                                                                                                                                                                               PRINTS; PR00262; IL1HBGF.
ProDom; PD000831; HB/F_gr
                                                                                                                                                                                                                                        InterPro; IPR002348; 1
Pfam; PF00167; PGF; 1
                                                                                                                                                                                                                                                                                                    MIM; 603891;
                                                                                                                                                                                                                                                                                                                        Cerrew;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                               modified and this statement
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Strausberg R.;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             SEQUENCE FROM N.A.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          "FGF-19, a novel fibroblast
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Gurney A.L.;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Foster J.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        SEQUENCE FROM N.A.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    NCBI_TaxID=9606;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        16-OCT-2001 (Rel.
16-OCT-2001 (Rel.
16-OCT-2001 (Rel.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   095750;
                                                                                                                                                                                                                                                                             InterPro;
                                                                                                                                                                                                                                                                                                                                            HSSP; P09038; 1BFG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            FISSUE=Colon
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      179 ---GILAPQP--
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               6-OCT-2001
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      SUBCELLULAR LOCATION: Secreted.
TISSUE SPECIFICITY: EXPRESSED (
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 SIMILARITY: BELONGS TO THE HEPARIN-BINDING GROWTH FACTORS FAMILY.
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AF110400; AAD45973.1; -.
BC017664; AAH17664.1; -.
  l Similarity
67; Conserv
                                                                                                                                                                                 SM00442; FGF; 1.
                                                                                                                                                                                                                                                                                                                      HGNC:3675; FGF19.
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                                                                                                                                                                                                                                                         IPR002209; HB/F_growthfact.
IPR002348; IL1_HBGF.
                                                                             23
216 AA;
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    Conservative
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Gu í
                                                                                                                                                                                         HB/F_growthfact;
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                                                                             24002 MW;
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Last annotation updat
tor-19 precursor (FGF-
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u Q., I
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  31;
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              Score 207; DB 1;
Pred. No. 9.9e-12;
                                                                                               POTENTIAL.
FIBROBLAST GROWTH FACTOR-19
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Craniata; Vertebrata; I
Catarrhini; Hominidae;
                                                                             E0BCBC9C220F9832 CRC64;
  Mismatches
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Hillan K.,
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  There are no restrictions
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  91;
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                                  Length 216;
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Indels
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44;
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Gaps
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HSSP; P09038; 1BFG.
MGD; MGI:95517; Fgf3.
InterPro; IPR002209; H
InterPro; IPR002348; I
                                                     EMBL; Y00848; CANCO, PIR; A23930; TVMST2.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          MOUSE
FGF3_MOUSE
                                                                                                                                                                                                                             family.",
1. Cell Sci. Suppl. 13:87-96(1990).
1. Cell Sci. Suppl. 13:87-96(1990).
1. FUNCTION: COULD BE INVOLVED IN EAR DEVELOPMENT.
1. INDUCTION: BY INTEGRATION OF MOUSE MAMMARY TUMOR VIRUS.
1. SIMILARITY: BELONGS TO THE HEPARIN-BINDING GROWTH FACTORS FAMILY.
                                                                                                                                                                                                                                                                                                           MEDLINE=91193291; PubMed=1964688;
Dickson C., Acland P., Smith R., Dixon M., Deed R., McAllan Malther M., Fuller-Pace F., Kiefer P., Peters G.;
"Characterization of int-2: a member of the fibroblast growt
                                                                                                                                                                                                                                                                                                                                                                                                                                "Multiple RNAs expressed from the int-
carcinoma cell lines encode a protein
                                                                                                                                                                                                                                                                                                                                                                                                                                                               SEQUENCE OF 1-73 FROM N.A. MEDLINE=88296404; PubMed=2841106; Smith R., Peters G., Dickson C.;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           MEDLINE=86247582; PubMed=3013624;
Moore R., Casey G., Brookes S., Dixon M., Pet
"Sequence, topography and protein coding pote
putative oncogene activated by mouse mammary
EMBO J. 5:919-924(1986).
                                                                                                          entities requires a license agreement (S or send an email to license@isb-sib.ch).
                                                                                                                                        use by non-profit institutions as long as modified and this statement is not removed. U
                                                                                                                                                                  This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBL outstation the European Bioinformatics Institute. There are no restrictions on it
                                                                                                                                                                                                                                                                                                                                                                                                                 growth factors.",
                                                                                                                                                                                                                                                                                                                                                                        CHARACTERIZATION.
                                                                                                                                                                                                                                                                                                                                                                                                     EMBO J. 7:1013-1022(1988).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    NCBI_TaxID=10090;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Bukaryota; Metazoa; Chordata;
Mammalia; Eutheria; Rodentia;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Mus musculus (Mouse)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                FGF3 OR FGF-3 OR INT-2.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                INT-2 proto-oncogene protein precursor
(FGF-3) (HBGF-3).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              01-NOV-1988
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                                                                           Y00848; CAA68767.1;
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(Rel. 09, Last sequence up)
(Rel. 41, Last annotation)
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ode a protein with ho
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Sciurognathi; Muridae;
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Murinae; Mus.
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HB/F

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RESULT
FGF3_HU
    DESCRIPTION OF COLUMN TO THE PROPERTY OF COL
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SEQUENCE
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SMART; SM00442; FGF; 1.

PROSITE; PS00247; HBGF FGF; 1.

Proto-oncogene; Growth factor; Mitogen; Signal; Glycoprotein.

SIGNAL 1 17 POTENTIAL.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                              MEDLINE=89239468; PubMed=2470007;
Brooks S., Smith R., Casey G., Dicke
"Sequence organization of the human
teratocarcinoma cells.";
                                                                                                                                                                                                                                   the Buropean Bioinformatics Institute. The use by non-profit institutions as long modified and this statement is not removed. entities requires a license agreement (See
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             SEQUENCE FROM N.A. TISSUE=Placenta;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Eukaryota; Metazoa;
Mammalia; Eutheria;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               01-OCT-1989 (Rel. 12, Last sequence update)
15-JUN-2002 (Rel. 41, Last annotation update)
INT-2 proto-oncogene protein precursor (Fibroblast
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01-OCT-1989
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                                                                                                Genew;
                                                                                                                                        EMBL; X14445; CAA32615.1;
PIR; S04742; S04742.
                                                                                                                                                                                                               entities requires a license agreement (s or send an email to license@isb-sib.ch).
                                                                                                                                                                                                                                                                                                                                 This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBL outstation -
                                                                                                                                                                                                                                                                                                                                                                                                                                                             Oncogene 4:429-436(1989)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  NCBI_TaxID=9606;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Homo sapiens (Human)
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InterPro; IPR002209; HB/F_growthfact
InterPro; IPR002348; IL1_HBGF.
Pfam; PF00167; FGF; 1.
                                                                       MIM; 164950; -
                                                                                                                      HSSP; P31371;
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                                                                                                                                                                                                                                                                                                                                                                                                            SIMILARITY: BELONGS
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           LYASDHYNAE-
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     IFGSHYFDPENCRFQHQTLENGYDVYHSPQYHFLVSLGRAKRAFLPGMNPP------
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 LYTATARNSYHLQIHKNGHVDGAPHQTIYSALMIRSEDAGFVVITGVMSRRYLCMDFRGN 101
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       - PYSQFLSRRNEIPLIHFNTPIPR-----RHTRSAEDDSERDPLNVLKPRARMTPAPA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    LYCAT---KYHLOLHPSGRVNGSLENSAYSILEITAVEVGVVAIKGLFSGRYLAMNKRGR 104
                                                                                         HGNC:3681; FGF3.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     63; Conserv
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Primates;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              27214 MW;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      13.48;
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TO THE HEPARIN-BINDING GROWTH FACTORS FAMILY.
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                                                                                                                                                                                                                                      agreement (See http://www.isb-sib.ch/announce/
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Score 182.5;
Pred. No. 1.9e
26; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    POTENTIAL.
INT-2 PROTO-ONCOGENE PROTEIN.
N-LINKED (GLCNAC. .)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Craniata; Vertebrata;
Catarrhini; Hominidae
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Dickson C.,
human int-2 c
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 70D94FD6A7837C79 CRC64;
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                                                                                                                                                                                                                                                                             There are no restrictions ng as its content is in
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  DB 1;
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RESULT
FGF3_XI
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Best Local
                     EMBL; Z25539; CAA80987.1; EMBL; X65237; CAA46341.1; -
PIR; S39582; S39582.
PIR; S25713; S25713.
HSSP; P31371; 1G82.
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01-JUN-1994 (Rel.
01-NOV-1997 (Rel.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     FGF3_XE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             CARBOHYD
SEQUENCE
                                                                                                                                                                                                                  Tammahill D., IBAACE H.V., Close M.J., Peters G., Sl
"Developmental expression of the Xenopus int-2 (FGF-
activation by mesodermal and neural induction.",
Development 115:695-702(1992).
-i- FUNCTION: POTENT MITOGEN AND TRANSFORMING AGENT.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       FGF3.
                                                                                                  entities requires a license agreement (S or send an email to license@isb-sib.ch).
                                                                                                                           the European Bioinformatics Institute. The use by non-profit institutions as long modified and this statement is not removed.
                                                                                                                                                                 This SWISS-PROT entry is copyright. It is produced through between the Swiss Institute of Bioinformatics and the EW
                                                                                                                                                                                                                                                                                                               SEQUENCE OF 39-137 FROM N.A.
                                                                                                                                                                                                                                                                                                                                        Kiefer P., Mathieu M., Close "FGF3 from Xenopus laevis."; EMBO J. 12:4159-4168(1993).
                                                                                                                                                                                                                                                                                                                                                                                                                                               Bukaryota; Metazoa; Chordata; Craniata; Vertebrata;
Amphibia; Batrachia; Anura; Mesobatrachia; Pipoidea,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Fibroblast growth
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                XENLA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   PROSITE; PS00247; HBGF FGF; 1.

Proto-oncogene; Growth factor; Mitogen; Signal; Glycoprotein SIGNAL 1 17 POTENTIAL.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         ProDom; PD000831; HB/F
SMART; SM00442; FGF; 1.
                                                                                                                                                                                                                                                                                                    TISSUE=Neurula
                                                                                                                                                                                                                                                                                                                                                                               MEDLINE=94038898; PubMed=8223431;
                                                                                                                                                                                                                                                                                                                                                                                           SEQUENCE FROM N.A.,
                                                                                                                                                                                                                                                                                                                                                                                                                  NCBI_TaxID=8355;
                                                                                                                                                                                                                                                                                                                                                                                                                                    Xenopodinae;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Xenopus laevis (African clawed frog).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       CHAIN
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                                                                                                                                                                                                                                                                                     MEDLINE=93048831; PubMed=1425349;
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                                                                                                                                                                                                          SIMILARITY: BELONGS TO THE HEPARIN-BINDING GROWTH FACTORS FAMILY.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 XENLA
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       LYCAT---KYHLOLHPSGRVNGSLENSAYSILEITAVEVGIVAIRGLFSGRYLAMNKRGR 104
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               LYTATARNSYHLQIHKNGHVDGAPHQTIYSALMIRSEDAGFVVITGVMSRRYLCMDFRGN 101
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             65
239 AA;
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                                                                                                                                                                                                                                                                                                                                                                                                                                 Xenopus.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 STANDARD;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      CEFVERIHELGYNTYASRLYRTVSSTPGARRQPSAERLWYVSVNGKGRP
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35, Last
factor-3
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                                                                                                                                                                                                                                                                                                                                                                                           AND PARTIAL SEQUENCE
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           26;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  annotation update)
precursor (FGF-3)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           sequence update)
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INT-2 PROTO-ONCOGENE PROT

N-LINKED (GLCNAC. .) (P.

8DBEF17D2B2E3C63 CRC64;
                                                                                                                                                                                                                                                                                                                                                                  J.M.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Score 180.5; DB 1
Pred. No. 2.8e-09;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 PRT;
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                                                                                                                                                                                                                                                                                                                                                                   Peters
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                                                                                                                                      There are no restrictions ng as its content is in
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                                                                                                                                                                                                                                                                                                                                                                                                                                            Pipoidea;
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                                                                                                                             Usage
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   (HBGF-3) (INT-2)
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                                                                                                                                                                                                                                                                                                                                                                   Dickson
                                                                                                                                                                                                                                                          3., Slack J.M.W.;
(FGF-3) gene:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                         Euteleostomi;
                                                                                                                                                                                                                                                                                                                                                                                                                                             Pipidae;
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                                                                                                                                                                    TEMBL
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                                                                                                                                                                               a collaboration
                                                                                                                              for
                                                                                                                                                                    outstation
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InterPro;

IPR002209; IPR002348;

HB/F_growthfact IL1_HBGF.

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RESULT
FGF5_RA
         PIN DER REPRESENTATION OF THE PROPERTY OF THE 
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Best Local
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    FGF5_RAT S
P48807; Q63402;
01-FEB-1996 (Re]
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    CARBOHYD
SEQUENCE
PROSITE; PS00247; HBGF FGF; 1.
Proto-oncogene; Growth factor; Mitogen; Signal; SIGNAL 17 POTENTIAL.
                                                                          PRINTS; PR00262; IL1HBGF.
ProDom; PD000831; HB/F growthfact;
SMART; SM00442; FGF; 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Biochim. Biophys. Acta 1306:31-33(1996).

-i- ALTERNATIVE PRODUCTS: 2 ISOFORMS, LONG FORM (SHOWN HERE) AND A SHORT FORM/FEGF-5S; ARE PRODUCED BY ALTERNATIVE SPLICING.

-i- SIMILARITY: BELONGS TO THE HEPARIN-BINDING GROWTH FACTORS FAMILY.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          01-FEB-1996 (Rel.
01-FEB-1996 (Rel.
15-JUN-2002 (Rel.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            ProDom; PD000831; HB/F-growthfact; 1.

SMART; SM00442; FGF; 1.

PROSITE; PS00247; HBGF-FGF; 1.

Growth factor; Mitogen; Signal; Glycoprotein.

SIGNAL 1 21
                                                                                                                                                                                                                                                                                                                                                                                                                                    This SWISS-PROT entry is copyright. It is produced through between the Swiss Institute of Bioinformatics and the EN
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                a novel truncated form of FGF-5.";
Biochim michael ....
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   MEDLINE=96201703; PubMed=8611621;
Hattori Y., Yamasaki M., Itoh N.;
"The rat FGF-5 mRNA variant gener
                                                                                                                                               InterPro; IPR002209; HB/F_growthfact.
InterPro; IPR002348; IL1_HBGF.
Pfam; PF00167; FGF; 1.
                                                                                                                                                                                                                                                                                                                     entities requires a license agreement (S or send an email to license@isb-sib.ch).
                                                                                                                                                                                                                                                                                                                                                                 use by non-profit institutions as long as modified and this statement is not removed. U
                                                                                                                                                                                                                                                                                                                                                                                                                the European Bioinformatics Institute.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             STRAIN-Wistar;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   SEQUENCE FROM N.A. (LONG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Eukaryota; Metazoa; Chordata; Mammalia; Eutheria; Rodentia;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Rattus norvegicus (Rat).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Fibroblast growth factor-5 FGF5 OR FGF-5.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          SIGNAL
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                NCBI_TaxID=10116;
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                                                                                                                                                                                                                         D64085; BAA10966.1; -. D64086; BAA10967.1; -. P09038; 1BFG.
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83
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    33, Created)
    33, Last sequence update)
    41, Last annotation update)
    factor-5 precursor (FGF-5)

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26984 MW;
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Pred. No. 4.3e-09;
6; Mismatches 63
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N-LINKED (GLCNAC. . .).
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Sciurognathi; Muridae,
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                                                                                                                                                                                                                                                                                                                                                                                                         There are no restrictions
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   alternative
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                           Alternative splicing
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FGF5_MOUSE
ID FGF5_MOUSE
AC P15656; 0888
DT 01-APR-1990
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                         between
the Euro
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DOMAIN
CARBOHYD
VARSPLIC
VARSPLIC
SEQUENCE
                                                This
                                                                  Submitted (JUL-1998) to the EMBL/GenBank/DDBJ databases.
-!- ALTERNATIVE PRODUCTS: 2 ISOFORMS; A LONG FORM (SHOWN HERE) AND A SHORT FORM/FGF-5S; ARE PRODUCED BY ALTERNATIVE SPLICING.
-!- SIMILARITY: BELONGS TO THE HEPARIN-BINDING GROWTH FACTORS FAMILY.
                                                                                                                                                               SEQUENCE FROM N.A. (S
                                                                                                                                                                                                                                                                                              SEQUENCE FROM N.A. (LONG ISOFORM).

MEDLINE=90201563; PubMed=2318343;

Hebert J.M., Basilico C., Goldfarb M., Haub O., Martin G.R.

"Isolation of cDNAs encoding four mouse FGF family members

characterization of their expression patterns during embryo
Dev. Biol. 138:454-463(1990).
                                                                                                                                                                                      "Expression of the murine fibroblast growth factor adult central nervous system."; adult central nervous system."; proc. Natl. Acad. Sci. U.S.A. 87:8022-8026(1990).
                                                                                                                                                                                                                                                                                                                                                                                                                                        01-APR-1990 (Rel. 14, Last 15-JUN-2002 (Rel. 41, Last Fibroblast growth factor-5
                                                                                                                                                                                                                                                              STRAIN=C57BL/
                                                                                                                                                                                                                                                                                                                                                                                           Eukaryota; Metazoa; Chordata;
Mammalia; Eutheria; Rodentia;
                                                                                                                                                                                                                                                                                                                                                                                                                              FGF5 OR FGF-5.
                                                                                                                              translates into a
                                                                                                                                          "An alternatively-spliced FGF-5
                                                                                                                                                                                                                                                  MEDLINE=91045929; PubMed=1700424;
                                                                                                                                                                                                                                                                                                                                                                               NCBI_TaxID=10090;
                                                                                                                                                                                                                                                                                                                                                                                                                    Mus musculus (Mouse)
                                                                                                                   activity.";
                                                                                                                                                                                                                                                                        SEQUENCE FROM N.A. (LONG ISOFORM)
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            European Bioinformatics Institute. The by non-profit institutions as long
                                               SWISS-PROT
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                                    the Swiss
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                                    entry is copyright.
                                                                                                                             partial agonist/antagonist
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Pred. No. 7.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   FIBROBLAST GROWTH POLY-SER.
N-LINKED (GLCNAC.
                                                                                                                                                                                                                                                                                                                                                                                           Craniata; Vertebrata; Euteleostomi; Sciurognathi; Muridae; Murinae; Mus
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   PRT;
 not removed.
                                                                                                                                          mRNA
                                                                                                                                                               Tomooka Y.,
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                                   Bioinformatics
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-> QIYR (IN SHORT ISOFORM)
ING (IN SHORT ISOFORM).
                                   It is produced through a collaboration
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(FGF-5)
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                    There are no
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Usage
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            its content
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                     restrictions
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P12034; 075846;
01-OCT-1989 (Rel
                                                                                                                                                                                                                                                                                                                                                                                                                                                                       CARBOHYD
VARSPLIC
VARSPLIC
SEQUENCE
                                     MEDLINE=91045929; PubMed=1700424;
Haub O., Drucker B., Goldfarb M.;
"Expression of the murine fibroblast growth
                                                                                                                                                                                                                     HUMAN
SEQUENCE FROM N.A.
                            adult central nervous system."
                                                                                                             Eukaryota; Metazoa; Chordata; Craniata; V
Mammalia; Eutheria; Primates; Catarrhini;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            EMBL;
                                                                    rissum=Brain stem;
                                                                               SEQUENCE FROM N.A.
                                                                                                                                 Homo sapiens (Human)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    SIGNAL 1
                                                                                                  NCBI_TaxID=9606;
                                                                                                                                                        Fibroblast
                                                                                                                                                                16-OCT-2001 (Rel.
15-JUN-2002 (Rel.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 DOMAIN
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InterPro; IPR002348; IL1_HBGF.
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B37360;
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; M37823; AAB02660.1;
; M37821; AAB02660.1;
; M37822; AAB02660.1;
                                                                                                                                                                                                                                                                                EDDSERDPLNVLKP--RARMTPAP
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an email to
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AAB02660.1; JOINED.
AAB02659.1; ALT_SEQ.
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(LONG ISOFORM)
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121
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             license agreement (See http://www.isb-sib.ch/announce/license@isb-sib.ch).
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                                                                                                                                                    annotation update)
precursor (FGF-5)
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FIBROBLAST GROWTH F
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MISSING (IN SHORT ISOFORM).
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No. 2.
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      Query Match
Best Local S
Matches 56
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EMBL; M23536; AAB60699.1; -.
EMBL; M23534; AAB60699.1; JOINED.
EMBL; M23535; AAB60699.1; JOINED.
EMBL; M23534; AAB60699.1; ALT_SEQ.
EMBL; M23534; AAB60698.1; ALT_SEQ.
EMBL; AB016517; BAA33738.1; -.
EMBL; AB016517; BAA33738.1; -.
EMBL; AB1199; TVHUE5.
                                                                                  CARBOHYD
VARSPLIC
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CONFLICT
CONFLICT
SEQUENCE
                                                                                                                                                                                                                                                                                                                         PRINTS; PR00262; IL1HBGF.
ProDom; PD000831; HB/F gr
SMART; SM00442; FGF; 1.
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InterPro; IPR002348; IL1_HBGF.
Pfam; PF00167; FGF; 1.
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                                                                                                                                                                                                        DOMAIN
                                                                                                                                                                                                                                                                   SIGNAL
                                                                                                                                                                                                                                                                                    PROSITE; PS00247; HBGF_FGF; 1.
Proto-oncogene; Growth factor;
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Genew; HGNC:3683; F
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            or send an email to license@isb-sib.ch)
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"The human FGF-5 oncogene encodes
fibroblast growth factors.",
Mol. Cell. Biol. 8:3487-3495(1988)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            J. Biol.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            activation-specific genes."
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de Vries C.J.M., van Achterberg T.A.E.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         SEQUENCE FROM
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activity.":
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           MEDLINE=89096942; PubMed=3211147;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  ALTERNATIVE PRODUCTS: 2 ISOFORMS; A LONG FORM (SHOWN HERE) AND A SHORT FORM/FGF-5S; ARE PRODUCED BY ALTERNATIVE SPLICING. SIMILARITY: BELONGS TO THE HEPARIN-BINDING GROWTH FACTORS FAMILY.
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uki S., Asada M., Tomooka Y.,
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29.8%;
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POLY-SER.
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PSGR -> LGA (IN REF. 2).
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                                                                                      Query Match
Best Local &
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SEQUENCE
                                                                                                                                                                 PROSITE; PS00247; HBGF FGF; 1.
Growth factor; Mitogen; Signal; Glycoprotein.
SIGNAL 1 19 POTENTIAL.
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                                                                                                                                                                                                                                                                                                                                                                                                                      Development 121:1399-1410(1995).
-i- FUNCTION: POTENT MITOGEN AND TRANSFORMING AGENT (BY
-i- SIMILARITY: BELONGS TO THE HEPARIN-BINDING GROWTH F
                                                                                                                                                                                                                                                                                                                                                                                                                                                                         STRAIN=Rhode Island red; TISSUE=Embryo; MEDLINE=95309122; PubMed=7789270; Mahmood R., Kiefer P., Guthrie S., Dickson C., Multiple roles for FGF-3 during cranial neural
                                                                                                                                                                                                        SMART;
                                                                                                                                                                                                                                                                                                                        or send
                                                                                                                                                                                                                                                                                                                                           modified and this statement is not removed
                                                                                                                                                                                                                                                                                                                                                                        the European Bioinformatics Institute.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                 chicken.";
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            SEQUENCE FROM N.A.
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InterPro; IPR002348; ILL_HBGF.
Pfam; PF00167; FGF; 1.
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NGHVDGA-PHQTIYSALMIRSEDAGFVVITGVMSRRYLCMDFRGNIFGSHYFDPENCRFQ 116
                        LVIWLLLLALLPEPRVPAATASPRAPRDAGGRGGVYEHLGGAPRRKLYCATKYHLQIHP 61
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                                                                                                                                                                                                                                                                                Z47555; CAA87635.1; -. P31371; 1G82.
                                                                                                                                                                                                     SM00442; FGF; 1.
                                                                                         Similarity
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PD000831; HB/F_growthfact;
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(Rel.
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25050 MW;
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Neognathae; Galliformes; Phasianidae; Phasiani
                                                                                       12.3%;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             annotation update)
precursor (FGF-3) (HBGF-3).
                                                                          18;
                                                                         Score 167; DB
Pred. No. 4.3e-
18; Mismatches
                                                                                                                       POTENTIAL.
FIBROBLAST GROWTH FACTOR-3.
N-LINKED (GLCNAC. ..) (POT.)
B15D41D1E551C5D5 CRC64;
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                                                                                                                                                                                                                                                                                                                                                                    There are no restrictions
                                                                                                   DB 1;
                                                                                       .3e-08;
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eural development
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RESULT 1'4
FGFB XENLA
ID FGFB XENL.
AC P48806;
01-FEB-1996 (-
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FGF3_BRARE
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Best Local (
                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Matches
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CHAIN
SEQUENCE
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01-FEB-1996 (Rel. 33, Last sequence update)
01-NOV-1997 (Rel. 35, Last annotation update)
Fibroblast growth factor-3 precursor (FGF-3)
FGF3 OR FGF-3.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           This SWISS-PROT entry is copyright. It is produced through a collab between the Swiss Institute of Bioinformatics and the EMBL outst the European Bioinformatics Institute. There are no restrictions use by non-profit institutions as long as its content is in modified and this statement is not removed. Usage by and for com
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Kiefer P., Strahle U., Mason I., Dickson C.;

"Secretion and mitogenic activity of zebrafish FGF3 reveal
intermediate properties relative to mouse and Xenopus homologues.";

Oncogene 12:1503-1511(1996).

-i- FUNCTION: POTENT MITOGEN AND TRANSFORMING AGENT (BY SIMILARITY).

-i- SIMILARITY: BELONGS TO THE HEPARIN-BINDING GROWTH FACTORS FAMILY.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Growth factor; Mitogen; Signal; Glycoprotein.
SIGNAL 1 18 POTENTIAL.
CHAIN 19 256 FIBROBLAST GROWT
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NCBI TaxID=7955;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  PRINTS; PR00262; IL1HBGF.
ProDom; PD000831; HB/F_growthfact; 1.
SMART; SM00442; FGF; 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        ZFIN; ZDB-GENE-980526-178; fgf3.
InterPro; IPR002209; HB/F growthfact..
InterPro; IPR002348; IL1_HBGF.
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Pred. No. 2.
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FIBROBLAST GROWTH FACTOR-3.
FIBROBLAST GROWTH FACTOR-3.
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(Rel. 33, Created

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RESULT 15
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Best Local Similarity
Matches 30; Conserv
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P48805;
01-FEB-1996
01-FEB-1996
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PROSITE; PS00247; HBGF_FGF; 1.
Growth factor; Mitogen; Signal.
                                                                  Eukaryota; Metazoa; Chordata;
Amphibia; Batrachia; Anura; M
                                                                                                                      01-FEB-1996 (Rel. 33, Created)
01-FEB-1996 (Rel. 33, Last sequence update)
16-OCT-2001 (Rel. 40, Last annotation update)
Fibroblast growth factor-4-I precursor (FGF-4
fibroblast growth factor I) (XBFGF-I).
Xenopus laevis (African clawed frog).
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PRINTS; PR00262; II1HBGF.
PRODom; PD000831; HB/F_growthfact;
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Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Amphibia; Batrachia; Anura; Mesobatrachia; Pipoidea; Pipidae;
                   NCBI_TaxID=8355
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               EMBL; X62594; CAA44480.1; -. HSSP; P31371; 1G82.
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Isaacs H.V., Tannahill D., Slack J.M.W.;
"Expression of a novel FGF in the Xenopus embryo. A new candidate
inducing factor for mesoderm formation and anteroposterior
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               InterPro; IPR002209; HB/F_growthfact.
InterPro; IPR002348; IL1_HBGF.
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16-OCT-2001 (Rel.
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SUBCELLULAR LOCATION: Secreted (Probable).
SIMILARITY: BELONGS TO THE HEPARIN-BINDING GROWTH FACTORS FAMILY.
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40, Last annotation update)
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FIBROBLAST GROWTH FACTOR-4-II.
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                                                                                           Craniata; Vertebrata;
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Growth factor; Mitogen; Signal SIGNAL 22 PCHAIN 23 187 F
SEQUENCE 187 AA; 21223 MW;
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ProDom; PD000831; HB/F_growthfact;
SMART; SM00442; FGF; 1.
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Pfam; PF00167; FGF; 1.
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   134
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Isaacs H.V., Tannahill D., Slack J.M.W.;
Expression of a novel FGF in the Xenopus embryo. A new candidate
                                                                                                                                          75
                                                                                                                                                                                              51 YHLQIHKNGHVDGAPHQTIYSALMIRSEDAGFVVITGVMSRRYLCMDFRGNIFGSHYFDP 110
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               FUNCTION: GOOD CANDIDATE FOR AN INDUCING FACTOR WITH POSSIBLE ROLES BOTH IN MESOBERM INDUCTION AT THE BLASTULA STAGE AND IN THE FORMATION OF THE ANTEROPOSTERIOR AXIS AT THE GASTRULA STAGE. SUBCELLULAR LOCATION: Secreted (Probable).

SIMILARITY: BELONGS TO THE HEPARIN-BINDING GROWTH FACTORS FAMILY.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Buropean Bioinformatics Institute. The by non-profit institutions as long
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EECKFKETLLPNNYNAYESRKYPGMYTALGKNGR
                                                              ENCREQUELENGYDVYHSPQY-HFLVSLGRAKR
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31.9%;
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Pred. No. 9.8e-07
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FIBROBLAST GROWTH FACTOR-4-I.
AAE63D65E82AD1BD CRC64;
                                                                                                                                                                                                                                                                       Mismatches
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Search completed: May 23, 2003, 07:43:46 Job time : 26 secs

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3: pir3:*
4: pir4:*
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A;Gene: fgf-23 C;Keywords: nu

nucleus

C; Genetics:

C; Comment: This factor, a secreted

protein, acts on proximal cells and plays roles

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ALIGNMENTS

RESULT JC7513

R;Yamashita, T.; Yoshioka, M.; Itoh, N.
Biochem. Biophys. Res. Commun. 277, 494-498, 2000
A;Title: Identification of a novel fibroblast growth fact A;Reference number: JC7513; MUID:20490027; PMID:11032749
A;Contents: Embryo

factor,

FGF-23,

preferentially exp

fibroblast growth factor-23 - mouse C;Species: Mus musculus (house mouse) C;Date: 30-Jun-2001 #sequence_revision 30-Jun-2001 #text_change 30-Jun-2001 C;Accession: JC7513

A;Accession: JC7513
A;Molecule type: mRNA
A;Residues: 1-251 <YAM>
A;Cross-references: DDBJ:AB037889

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transforming protein (int-2) - mouse (;Speciles: Mus musculus (house mouse) (;Speciles: Mus musculus (house mouse) (;Cpeciles: Albec-1989 #sequence_revision 31-Dec-1989 #text_change 18-Jun-1999 C;Accession: A23930; 808157 R;Moore, R.; Casey, G.; Brookes, S.; Dixon, M.; Peters, G.; Dickson, C.
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                                                                                                                                                                              PEGCRPFAKFI 251
                                                                                                                                                                                                                                           AEDDSERDPLNVLKPRARMTPAPASCSQELPSAEDNSPMASDPLGVVRGGRVNTHAGGTG 240
                                                                                                                                                                                                                                                                           ENGYDYYLSQXHHYLVSLGRAKKIFQPGTNPPPFSQFLARRNEVFLLHFYTVRPRRHTRS
                                                                                                                                                                                                                                                                                                          ENGYDVYHSPQYHFLVSLGRAKRAFLPGMNPPPYSQFLSRRNEIPLIHFNTPIPRRHTRS 180
                                                                                                                                                                                                                                                                                                                                           VDGTPHQTIYSALMITSEDAGSVVITGAMTRRFLCMDLHGNIFGSLHFSPENCKFRQWTL 120
                                                                                                                                                                                                                                                                                                                                                                          VDGAPHQTIYSALMIRSEDAGFVVITGVMSRRYLCMDFRGNIFGSHYFDPENCRFQHQTL 120
                                                                                                                                                                                                                                                                                                                                                                                                        AEDPPERDPLNVLKPRPRATPVPVSCSRELPSAEEGGPAASDPLGVLRRGRGDARGGAGG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         70.7%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                          25;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Score 961; DB 2;
Pred. No. 5.4e-80;
5; Mismatches 49
                                                                                                                                                                                                                                                                                                                                                                                                                                                                          49;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Length
                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         251;
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A;Map position: 11q13.3-11q13.3
A;Introns: 74/1; 108/3
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                묽
                                                                                                                                                                                                                                                                                                                                                                                                                                                       N;Alternate names:
C;Species: Homo sap
C;Date: 10-Sep-1999
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         밁
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                                                                                                                                                                                                                                                                                                                                                                                             R;Brookes, S.; Smith, R.;
Oncogene 4, 429-436, 1989
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         문
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       fibroblast growth factor 3 precursor - human N;Alternate names: transforming protein int-2
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    A; Map position: 7
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                A;Cross-references: GB:Y00848; GB:M26284; GB:X68450; NID:g52716; PIDN:CAA68767.1; R;Acland, P.; Dixon, M.; Peters, G.; Dickson, C.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Nature 343,
                                                                                                                ;1-17/Domain: signal sequence ;18-239/Product: transforming
                                                                                                                                                                                                                                                Gene: GDB:FGF3; INT2
                                                                                                                                                      Superfamily: fibroblast growth factor Keywords: growth factor
                                                                                                                                                                                                                                                                                                                                                     ;Title: Sequence organization of the human int-2 gene and Reference number: S04742; MUID:89239468; PMID:2470007
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Matches
                                                              Query Match
Best Local
                                                                                                                                                                                                                                                                             Cross-references: EMBL:X14445; NID:g33937; PIDN:CAA32615.1;
                                                                                                                                                                                                                                                                                                    Molecule type: DNA
Residues: 1-239 <BRO>
                                                                                                                                                                                                                                                                                                                                                                                                                                             Date: 10-Sep-1999 #sequence_revision 10-Sep-1999 #text_change
                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Species: Homo sapiens (man)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          :Introns: 74/1; 108/3
:Superfamily: fibroblast growth factor
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        ;Molecule type: mRNA
:Residues: 'HSRAGLARGRVLPAPRLRETRAGAAAAAGGRDAGM',3-17
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             ;Molecule type: DNA;
;Residues: 1-245 <MO
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            ;Title: Sequence, topography and protein coding potential of mouse int-2: a putative ;Reference number: A23930; MUID:86247582; PMID:3013624;Accession: A23930
                                                                                                                                                                                                                                                                                                                                            Accession: S04742
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Gene: int-2
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Status: not compared with conceptual translation
                                                                                                                                                                                                                                                                                                                                                                                                                                   Accession: S04742
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Query Match
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  162
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             105 LYASDHYNAE-CEFVERIHELGYNTYASRLYRTGSSGPGAQRQ--PGAQRPWYVSVNGKG 161
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 102 IFGSHYFDPENCRFQHQTLENGYDVYHSPQYHFLVSLGRAKRAFLPGMNPP-----
           42
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Local Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 5, 919-924, 1986
LYTATARNSYHLQIHKNGHVDGAPHQTIYSALMIRSEDAGFVVITGVMSRRYLCMDFRGN 101
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        RPRRGFKTRRTQKSSLF----LPRVLGHKDHEMVRLLQSSQPRAPGEGSQPRQR-----
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    --RQKKQSPGDHGKM--ETLSTRATPSTQLHTGG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        SCSQELPSAEDNSPMASDPLGVVRGGRVNTHAGG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             -PYSQFLSRRNEIPLIHENTPIPR-----RHTRSAEDDSERDPLNVLKPRARMTPAPA 204
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        LYCAT --- KYHLQLHPSGRVNGSLENSAYSILEITAVEVGVVAIKGLFSGRYLAMNKRGR 104
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             growth factor; transforming
                                                              Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            1-245 <MOO>
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Conservative
                                                                                                                                                                                                                                                                                                                                                                                                             R.; Casey, G.; Dickson, C.; Peters, G.
                                                           13.3%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       13.4%;
29.4%;
                                                                                                                  protein
                                                                                                                                 #status
                                           26;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Score 182.5; |
Pred. No. 4.2e
26; Mismatches
                                                             Score 180.5;
Pred. No. 6.
                                                                                                            predicted <SIG>
(int-2) #status predicted <MAT>
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                                        6.1e-09;
ches 75;
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                                                                              DB 1;
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                                                                          Length 239;
                                      Indels 15;
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Biochim. Biophys. Acta 1306, 31-33, 1996
A;Title: The rat FGF-5 mRNA variant generated
A;Reference number: S68144; MUID:96201703; PMJ
                                                                                                 A;Reference number: A;Accession: S68144
                                         A; Molecule type: mRNA
A; Residues: 1-266 < HAT>
                                                                                                                                                                               R;Hattori,
                                                                                                                                                                                                              C;Date: 06-Dec-1996 #sequence_revision 13-Mar-1997
                                                                                                                                                                                                                                         fibroblast
C;Species:
                                                                                                                                                                                                                                                                                 S68144
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                      A;Cross-references:
                                                                            A;Status: preliminary; nucleic acid sequence not
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A; Residues: 39-137 <TANN
A; Cross-references: EMBL: X65237; NID: 964855;
A; Cross-references: EMBL: X65237; NID: 964855;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      A;Cross-references: EMBL:Z25539; NID:g396830; PIDN:CAA80987.1; R;Tannahill, D.; Isaacs, H.V.; Close, M.J.; Peters, G.; Slack, Development 115, 695-702, 1992
A;Title: Developmental expression of the Xenopus int-2 (FGF-3) A;Reference number: S25713; MUID:93048831; PMID:1425349
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A;Residues: 1-237 <KIE>
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                A; Title: FGF3 from Xenopus laevis
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      R; Kiefer,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  C; Species: Xenopus laevis (African
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  N; Alternate names: FGF-3 protein; fibroblast
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       transforming protein int-2 - African clawed frog
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                A; Molecule type: mRNA
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                                                                                                                                                                                                                                                                                                                                                                                                       153
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                                                                                                                                                                                                                                                                                                                                                                                                                                      123 RLYASETYNPE-CEFVERIHELGYNTYASRLYRTVPSGAGTKRKASAERLWYVSINGKGR
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2, 4159-4168, 1993
                                                                                                                                                                                                                                                                                                                                                             PRRGFKTRRTOKSSLFLPRVLDNKDHDAVRLFHTNAVYRES-
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      LYCAT----KYHLQIHLNGKINGTLEKNSVFSILEITAVDVGIVAIKGLFSGRYLAMNQRG 122
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                                                                                                                                                                                                                                       growth factor 5 - rat
Rattus norvegicus (Norway rat)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               55
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fibroblast
                                                                                                                                                                               Yamasaki, M.; Itoh, N.
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                    EMBL: D64085;
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growth
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  NID:g992952; PIDN:BAA10966.1; factor
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Score 178.5; DB 1
Pred. No. 9.2e-09;
6; Mismatches 63
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                clawed
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                                                                                                                     PMID:8611621
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                                                                                                                                        alternative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       63;
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                                                                                                                                    splicing
              PID:g992953
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J.M.W.
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                                                                                                                                      encodes
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                                                                                                                                    novel
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fibroblast growth factor 5 - hun N; Alternate names: transforming C; Species: Homo sapiens (man)
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TVHUF5
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A;Residues: 1-264 <HAU>
A;Cross-references: GB:M37821; GB:M37822; GB:M37823; NID:g193280; R;Hebert, J.M.; Basilico, C.; Goldfarb, M.; Haub, O.; Martin, G.R. Dev. Biol. 138, 454-463, 1990
Dev. Biol. 138, 454-463, 1990
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   A; Molecule type: mRNA
A; Residues: 1-264 < HEB>
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A36207
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Best Local S
Matches 57
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          ev. Biol. 138, 454-463, 1990
;Title: Isolation of cDNAs encoding four mouse FGF family members and
;Reference number: A37360; MUID:90201563; PMID:2318343
                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Cross-references: GB:M30643; NID:g193294;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Status: preliminary
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Best Local Similarity
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                                                                                                                                                                                                                  -----PQYHFLVSLGRAKRAFLPGMNPPPYS-QFLSR--RNEIPLIHFNTPIPRRHTRSA 181
                                                                                                                                                                                                                                                                                                                                                        ASPLLGSSWGGLIH---LYTATARNS-----YHLQIHKNGHYDGAPHQTIYSALM 74
                                                                                                                                                                                  EKTGREWYVALNKRGKAKRGCSPRVKPQHVSTHFLPRFKQSEQPELSFTVTVP------
                                                                                                                                                                                                                                                      IFAVSQGIVGIRGVFSNKFLAMSKKGKLHASAKF-TDDCKFRERFQENSYNTYASAIHRT
                                                                                                                                                                                                                                                                                      IRSEDAGFYVITGYMSRRYLCMDFRGNIFGSHYFDPENCRFQHQTLENGYDVYHS-----
                                                                                                                     --EKKKPPVKPKVPLSQPRRSPSP
                                                                                                                                                    EDDSERDPLNVLKP--RARMTPAP 203
                                                                                                                                                                                                                                                                                                                          ASP--GSQGSGSEHSSFQWSPSGRRTGSLYCRVGIGFHLQIYPDGKVNGSHEASVLSILE 120
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         IRSEDAGFVVITGYMSRRYLCMDFRGNIFGSHYFDPENCRFQHQTLENGYDVYHS----- 129
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              ASP--GSQGSGSEHSSFQWSPSGRRTGSLYCRVGIGFHLQIYPDGKVNGSHEASVLSILB 120
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                                                                                                                                                                                                                                                                                                                                                                                                                 Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                   fibroblast
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28.2%;
                                human
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              protein
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                 factor
                                                                                                                                                                                                                                                                                                                                                                                                             Score 171; DB 2;
Pred. No. 5.1e-08;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Score 176.5; DB 2
Pred. No. 1.6e-08;
                                                                                                                   254
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                FGF5
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                                                                                                                                                                                                                                                                                                                                                                                               72;
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                                                                                                                                                                                                                                                                                                                 A;Status: preliminary; translated A;Molecule type: mRNA A;Residues: 1-220 <MAH>
                                                                                                                                                                                                                                                                                                                                                                                   Development 121, 1399-1410, 1995
A; Title: Multiple roles for FGF-3 during c
A; Reference number: ISOS88; MUID:95309122;
                                                                                                                                                                                                                                                                                                                                                                                                                                                        fibroblast growth factor 3 - chicken C;Species: Gallus gallus (chicken) C;Date: 13-Sep-1996 #sequence_revision 13-Sep-1996 #text_change C;Accession: I50588
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                                                                                                                                                                                                                                                                                                                                                                        A; Accession:
                                                                                                                                                                                                                                                                                                                                                                                                                                      R; Mahmood, R.; Kiefer, P.; Guthrie,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                I50588
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  RESULT 8
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C; Superfamily: fibroblast growth factor
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          A; Zhan, X; Bates, B.; Hu, X.; Goldfarb, M.

Mol. Cell. Biol. 8, 3487-3495, 1988

A; Title: The human FGF-5 oncogene encodes a novel protein

A; Reference number: A31194; MUID:89096942; PMID:3211147
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            A; Molecule type: mRNA
A; Residues: 1-267 < ZHA>
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                                                                                                                                   2 LVIWLLLLALLPEPRVPAATASPRAPRDAGGRGGVYEHLGGAPRRRKLYCATKYHLQIHP
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                                                                                                                                                                      6 LRLW--VCALCSVCSMSVLRAYPNASPLLGSSWGGLIHLYTATAR-----NSYHLQIHK 57
 ERIHELGYNTYASRLYRTVPSGASTKR
                                                                                               NGHVDGA-PHQTIYSALMIRSEDAGFVVITGVMSRRYLCMDFRGNIFGSHYFDPENCRFQ 116
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                                HOTLENGYDVYHSPQYHFLVSLGRAKR
                                                                  GGKINGTLEKNSVFSILEITAVDVGIVAIKGLFSGRYLAMNKRGRLYASENYNTE-CEFV
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           SAMSSSSASSSPAAS--LGSQGSGLEQSSFQWSLGARTGSLYCRVGIGFHLQIYPDGKVN
                                                                                                                                                                                                             49;
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bblast growth factor
                                                                                                                                                                                                        12.3%; Score 167; DB 2; I
33.3%; Pred. No. 9.3e-08;
Mismatches 70;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          27; Mismatches
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Pred. No. 7.9e-08;
                                                                                                                                                                                                                                                                                                                                                     from GB/EMBL/DDBC
                                                                                                                                                                                                                                                                                                                                                                                                                                        S.; Dickson, C.; Mason,
                                  143
147
                                                                                                                                                                                                                                                                                                                                                                                     cranial neural 2; PMID:7789270
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RESULT

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embryonic fibroblast growth factor II - African clawed frog (;Species: Kenopus laevis (African clawed frog) C;Date: 06-Sep-1996 #sequence_revision 13-Mar-1997 #text_change 17-Mar-2000 C;Accession: S54407 R;Isaacs, H.V.; Tannahill, D.; Slack, J.M.W. Development 114, 711-720, 1992
      embryonic fibroblast growth factor - African clawed frog C;Species: Xenopus laevis (African clawed frog) C;Date: 19-Feb-1994 #sequence_revision 10-Nov-1995 #text_change C;Accession: S23595 R;Isaacs, H.V.; Tannahill, D.; Slack, J.M.W.
                                                                                                                   S23595
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        A;Introns: 93/2; 127/3
C;Superfamily: fibroblast growth factor
C;Keywords: embryo; fibroblast; growth
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           R;Kiefer, P.; Straehle, U.; Dickson, C. Gene 188, 211-215, 1996
A;Title: The zebrafish Fgf-3 gene: cDNA sequence, transcript A;Reference number: JC4627; MUID:96194899; PMID:8854946
A;Accession: JC4627
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  A;Molecule type: mRNA
A;Residues: 1-256 <KIE>
A;Cross-references: EMBL:Z48714; NID:g971333; PIDN:CAA88596.1; PID:g971334
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      C;Date: 10-May-1996 #sequence_revision 19-Jul-1996 #text_change 16-Jul-1999 C;Accession: JC4627
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      A; Accession: S54407
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              A;Gene: Fgf-3
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           A; Experimental source: embryo
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 fibroblast growth factor 3 - zebra fish C;Species: Brachydanio rerio (zebra fish)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Cross-references: EMBL:X62594;
Superfamily: fibroblast growth
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Molecule type: mRNA
Residues: 1-192 <ISA>
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Status: preliminary
                                                                                                                                                                                                                                                                                                                                                                                                                                Query Match
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                                                                                                                                                                                                                                              111 ENCRFOHOTLENGYDVYHSPQY-HFLVSLGRAKR 143
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             123 RLYASEVFNRE-CEFLERIHELGYNTYAS-RHHATT-
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    101 NIFGSHYFDPENCRFQHQTLENGYDVYHSPQYHFLVSLGRAKRAFLPGMNPPP
                                                                                                                                                                                                                                                                                                08
                                                                                                                                                                                                                                                                                                                                51 YHLQIHKNGHVDGAPHQTIYSALMIRSEDAGFYVITGVMSRRYLCMDFRGNIFGSHYFDP 110
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    66
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      42 LYTATARNSYHLQIHKNGHVDGA-PHQTIYSALMIRSEDAGFVVITGVMSRRYLCMDFRG 100
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Local
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                                                                                                                                                                                                                                                                                            FHIQVLPDGRINGMHNENRYSLLEISPVEVGVVSLYGIKSAMFVAMNAKGKLYGSRYFN- 138
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             LYCAT---KYHLQIHPNGKIDGSLEENNPLSILEITAVDVGVVAIKGLFSGRYLAMNEKG 122
                                                                                                                                                                                                                                                                                                                                                                                       30;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                      NID:g840919; factor
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Pred. No. 5.5e-07;
3; Mismatches 39
                                                                                                                                                                                                                                                                                                                                                                              Score 155; DB 2;
Pred. No. 9.7e-07;
5; Mismatches 37
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            factor
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           PIDN: CAA44480.1;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        PID:9840920
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             160
                                                  16-Jul-1999
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$20102
fibroblast growth factor 6 precursor - human
N,Alternate names: fibroblast growth factor-related
C;Species: Homo sapiens (man)
C;Date: 18-Feb-1994 #sequence revision 12-Apr-1996
C;Accession: $20102; $23739; $04204; $36910
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RESULT 12
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A;Title: A positive feedback loop coordinates growth and A;Reference number: 150710; MUID:95021713; PMID:7935794
A;Accession: $50858
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               submitted to the EMBL Data A; Reference number: $78506
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 fibroblast growth factor 4 - chicken C;Species: Gallus gallus (chicken) C;Date: 13-Sep-196 #sequence revision C;Accession: S78506; S50858; T50710
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                                                                                                                                                                                                                                                                            C; Keywords:
                                                                                                                                                                                                                                                                                                                                                                   A;Molecule type: DNA
A;Residues: 1-136,'Q',137-194,'I' <NIW>
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     R;Niswander,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     A;Cross-references: EMBL:X62593; C;Superfamily: fibroblast growth
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     A; Molecule type: mRNA
A; Residues: 1-187 < ISA>
                                                                                                                                                                                                                                                                                                                                                 A;Cross-references: EMBL:U14654; NID:g609347;
                                                                                                                                                                                                                                                                                                                                                                                                     A;Status: nucleic
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                C; Accession:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Development 114, 711-720, 1992
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        A;Cross-references: EMBL:U14654; NID:g609347; PIDN:AAA58706.1; PID:g609348
R;Niswander, L.; Jeffrey, S.; Martin, G.R.; Tickle, C.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              A;Residues: 1-194 <NIS>
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                A;Accession: S78506
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              A; Molecule type:
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                                                                                                                                                                                                           Matches
                                                                                                                                                                                                                                                                                             Superfamily: fibroblast growth factor
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149
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LLPNNYNAYESRIYPGMYIALSKNGRTKKGNKVSPTMTVTHFLP
                            TLENGYDVYHS----PQYHFLVSLGRAKRA---
                                                                                                 GHVDGAPHQTIYSALMIRSEDAGFVVITGVMSRRYLCMDFRGNIFGSHYFDPENCRFQHQ 118
                                                                                                                                                                      GARLRIWVCALC--SVCSMSVLR--AYPNASPLLGSSWGGLIHLYTATARNSYHLQIHKN 58
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                YHLQIHKNGHVDGAPHQTIYSALMIRSEDAGFVVITGVMSRRYLCMDFRGNIFGSHYFDP 110
                                                                GRIDGIHSENRYSLLEISPVERGVVSIFGVRSGLFVAMNSKGKLYGSTHVNDE-CKFKEI
                                                                                                                                     GPRQRRWDAALFARSVARLPAERRDAARDGDYLLG--YKRLRRLY-CNVGIGFHIQVLPD
                                                                                                                                                                                                          51;
                                                                                                                                                                                                                                                                            growth factor; transforming protein
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      30;
                                                                                                                                                                                                                          Similarity
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                                                                                                                                                                                                          22; Mismatches
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                                                                                                                                                                                                                          Score 146.5;
Pred. No. 5.9
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Pred. No. 2.2e-06;
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; PMID:1618138
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                                                                                                                                                                                                                          .9e-06;
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                                                                                                                                                                                                                                              DB
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                              FLP 147
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factor-related

protein FGF.6; transforming

#text_change

21-Jul-2000

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A;Title: Isolation and sequence of the murine Fgf6 cDNA A;Reference number: I49664; MUID:93120244; PMID:1477139 A;Accession: I49665
                                                                                                                                     A;Molecule type: DNA
A;Residues: 1-208 <LAP>
A;Cross-references: EMBL:X51552
                                                                  R;Ollendorff, V.; Rosnet, O.; Marics, Biochimie 74, 1035-1038, 1992
                                                                                   A;Note: it is uncertain whether Met-1 or Met-11 is the initiator R;Ollendorff, V.; Rosnet, O.; Marics, I.; Birnbaum, D.; deLapeyr
                                                                                                                                                                                                            A; Reference number: S14192;
A; Accession: S14192
                                                                                                                                                                                                                                                    Oncogene 5, 823-831
A; Title: Structure,
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       R;Coulier, F.; Batoz, M.; Marics, I.; de Lapeyriere, O.; Birnbaum, D. Oncogene 6, 1437-1444, 1991
A;Title: Putative structure of the FGF6 gene product and role of the signal A;Reference number: S20102; MUID:91360279; PMID:1886714
A;Accession: S20102
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A;Cross-references: EMBL:X14071; NID:g31354; PIDN:CAB37648.2;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            A; Title: Characterization of the HST-related FGF.6 gene, A; Reference number: 804204; MUID:89201880; PMID:2649847
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      A; Note: it is uncertain whether Met-1, Met-11 or Met-34; R; Iida, S.; Yoshida, T.; Naito, K.; Sakamoto, H.; Katoh, Oncogene 7, 303-309, 192
A; Title: Human hst-2 (FGF-6) oncogene: cDNA cloning and A; Reference number: S23739; MUID:92195660; PMID:1549352
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               A; Cross-references: EMBL: X57075
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          A; Molecule type: DNA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          A; Accession: S23739
                                                                                                                                                                                                                                                                                                                  ;Species: Mus musculus (house mouse)
;Date: 21-Nov-1993 #sequence revision 10-Nov-1995 #text_change 17-Mar-2000
;Accession: S14192; I49655; I49664
                                                                                                                                                                                                                                                                                                 Accession: S14192; I49665; I49664; de Lapeyriere, O.; Rosnet, O.; Benharroch,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                ;41-208/Product: fibroblast growth factor 6 #status predicted <MAT>
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Superfamily: fibroblast growth factor 1-40/Domain: (or 11-40 or 34-40) signal sequence #status predicted
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      ;Cross-references:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      ;Molecule type:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   ;Cross-references: EMBL:X63454
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     ;Residues: 1-208 <COU>
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Query Match
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               ;Molecule type: mRNA;Residues: 1-208 <III
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Status: not compared with conceptual
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                184 SKYGRVKRGSKVSPIMTVTHFLP
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                136 VSLGRAKRA----
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             125
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Match 10.4%; Score 141.5; DB 2 Local Similarity 28.7%; Pred. No. 1.8e-05;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        ASPLLGSSW--GGLI------HLYTATARNSYHLQIHKNGHVDGAPHQTIYSALMIRSED 79
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   RGVVSLFGVRSALFVAMNSKGRLYATPSFQ-EECKFRETLLPNNYNAYESDLYQGTYTAL
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                AGFVVITGVMSRRYLCMDFRGNIFGSHYFDPENCRFQHQTLENGYDVYHSPQYH----FL 135
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              AGEIAGVNWESGYLVGIKRQRRLY-CNVGIGFHLQVLPDGRISGTHEENPYSLLEISTVE 124
                                                                                                                                                                                                                                                                                                                                                                                            growth factor 6 - mouse
                                                                                                                                                                                                                                                                              823-831,
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                                                                                                                                                                                                                               chromosome mapping and S14192; MUID: 90295275;
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                                                                                                                                                                                                                                                                            1990
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           -----FLP 147
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        21; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              206
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                                                                                                                                                                                                                                 expression of PMID:2193291
                                                                                                                                                                                                                                                                                             D.; Raybaud, F.; Marchetto, S.;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       DB 2;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             56;
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                                                                                     deLapeyriere,
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RESULT 15
JC4268
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A;Note: The authors translated the codon GGC for residue C;Comment: This protein is a member of fibroblast growth
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      N;Alternate names: transforming protein hst
C;Species: Bos primigenius taurus (cattle)
C;Date: 10-Nov-1995 #sequence_revision 08-Feb-1996 #text_change 17-Mar-2000
                                                                                                                                                                                                           C; Keywords: thymus; transforming protein
                                                                                                                                                                                                                                                                                                                                                                                                      A; Title: An unexpected transforming gene in calf-thymus A; Reference number: JC4268; MUID:96032369; PMID:7557455
                                                                                                                                                                                                                                                                                                                                                                                                                                                           C;Accession: JC4268
R;Yu, J.C.; DeSeabra, A.J.J.; Wang,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         밁
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                                                                                                                                                                                                                                                                                                                                                       A; Residues: 1-206 < YUJ>
                                                                                                                                                                                                                                                                                                                                                                                          A; Accession: JC4268
                                                                                                                                                                                                                                                                                                                                                                                                                                            Gene 162, 333-334, 1995
                                                                                                                                                                                                                                                 A;Introns: 113/3; 145/2
                                                                                                                                                                                                                                                                   A;Gene:
                                                                                                                                                                                                                                                                                                                                                                        A; Molecule type: mRNA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   fibroblast growth factor 4 -
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       C; Superfamily:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         A; Introns: 116/1;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        A;Gene: Fgf6
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              A;Molecule type: DNA
A;Residues: 1-18 <RE2>
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              A;Status: preliminary; translated from GB/EMBL/DDBJ
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  A;Residues: 19-208 <RES>
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   A;Status: preliminary; translated from GB/EMBL/DDBJA;Molecule type: mRNA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  A;Accession: I49664
                                                                                                                                                                                                                         Superfamily: fibroblast growth factor
                                                                                                                                                                            Query Match
                                                                                                                                                                                                                                                                                   Genetics:
                                                                                                                                            Matches
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Best Local Similarity
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Cross-references:
     154
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                                                                                                                                                            Local
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                                                                                                   YHLQIHKNGHVDGAPHQTIYSALMIRSEDAGFVVITGVMSRRYLCMDFRGNIFGSHYFDP 110
E-CRFREILLPNNYNAYECDRHPGMFIALSKNGKAKKGNRVSPTMKVTHFLP
                                    ENCREQUOTLENGYDVY ----HSPQYHFLVSLGRAKRA ---
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         SKYGRVKRGSKVSPIMTVTHFLP
                                                                  FHLQVLPDGRIGGVHADTSDGLLELSPVERGVVSIFGVASRFFVAMSSRGRLYGSPFFTD 153
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         AGFVVITGVMSRRYLCMDFRGNIFGSHYFDPENCRFQHQTLENGYDVYHSPQYH----FL 135
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             AGEISGVNWESGYLVGIKRORRLY-CNVGIGFHLOVPPDGRISGTHEENPYSLLEISTVE 124
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               ASPLIGSSW--GGLI-----HLYTATARNSYHLQIHKNGHVDGAPHQTIYSALMIRSED 79
                                                                                                                                          36;
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                                                                                                                                                            Similarity
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             GB:M92416; NID:g193288; PIDN:AAA62261.1; PID:g666915
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                                                                                                                                          16;
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                                                                                                                                       Score 138; DB 2;
Pred. No. 3.8e-05;
6; Mismatches 44
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Score 138.5;
Pred. No. 3.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                           L.M.; Fleming,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Mismatches
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                                                                                                                                                                                                                                                                                                                                                                                                                                                           T.P.;
                                                                                                                                                                       Length 206;
                                                                                                                                        Indels
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factor
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                                  --FLP 147
204
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                                                                                                                                     Gaps
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Search completed: May Job time : 21 secs

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Minimum DB seq length: 0
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Perfect score:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Post-processing: Minimum Match 0%
Maximum Match 10
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1360
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                                                                                                                                                                                                                                                                                                                                                                                                                  Published_Applications
                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Maximum Match 100%
Listing first 45 summaries
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           GenCore version 5.1.4 p5_4578 Copyright (c) 1993 - 2003 Compugen Ltd.
                                                                                                                                                                                                                               /cgm2_6/ptodata/2/pubpaa/US08_NEW_PUB.pep:*
/cgm2_6/ptodata/2/pubpaa/PCT_NEW_PUB.pep:*
/cgm2_6/ptodata/2/pubpaa/US06_NEW_PUB.pep:*
/cgm2_6/ptodata/2/pubpaa/US06_PUBCOMB.pep:*
/cgm2_6/ptodata/2/pubpaa/US07_NEW_PUB.pep:*
/cgm2_6/ptodata/2/pubpaa/US07_NEW_PUB.pep:*
'3gn2_6/ptodata/2/pubpaa/US09_PUBCOMB.pep:*

2gn2_6/ptodata/2/pubpaa/US09_NEW_PUB.pep:*

(2gn2_6/ptodata/2/pubpaa/US09_PUBCOMB.pep:*

/cgn2_6/ptodata/2/pubpaa/US10_NEW_PUB.pep:*

/cgn2_6/ptodata/2/pubpaa/US10_PUBCOMB.pep:*

/cgn2_6/ptodata/2/pubpaa/US60_NEW_PUB.pep:*

/cgn2_6/ptodata/2/pubpaa/US60_PUBCOMB.pep:*
                                                                                                                                                                                                       6/ptodata/2/pubpaa/PCTUS_PUBCOMB.pep:*
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Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match Length	ength DB	<u>.</u> π	ID	Description
ь	1360	100.0	. 251	9 !	US-09-901-938-2	Sequence
N	1360	100.0	251	φ	US-09-992-598-511	Sequence
ω	1360	100.0	251	Φ	US-09-989-293A-511	Sequence
4	1360	100.0	251	9	US-09-989-735-511	Sequence
ر ت	1360	100.0	251	9	US-09-990-444-511	Seguence
6	1360	100.0	251	9	US-09-989-730-511	Sequence
7	1360	100.0	251	9	US-09-990-436-511	Sequence
80	1360	100.0	251	φ	US-09-991-181-511	Seguence
9	1360	100.0	251	9	US-09-993-687-511	Sequence
10	1360	100.0	251	9	US-09-989-734-511	Seguence
11	1360	100.0	251	9	US-10-028-072-266	Sequence
12	1360	100.0	251	9	US-09-997-653-511	Sequence
13	1360	100.0	251	9	US-09-993-667-511	Sequence
14	1360	100.0	251	φ	US-10-121-049-266	Sequence
15	1360	100.0	251	φ	US-10-123-904-266	Sequence
16	1360	100.0	251	9	US-10-140-470-266	Sequence
17	1360	100.0	251	9	US-09-924-340-26	Seguence
18	1360	100.0	251	φ	US-09-990-438-511	Sequence
19	1360	100.0	251	9	US-09-990-562-511	Sequence

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Best Local Similarity
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SOFTWARE: PatentIn ver
SEQ ID NO 2
LENGTH: 251
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                                                                                                                                                                                                                                                                                                                                      Matches 251;
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APPLICANT: WHITE, Kenneth
APPLICANT: STROM, Tim
APPLICANT: MEITINGER, Thomas
TITLE OF INVENTION: NOVEL FIBROBLAST GROWTH FACTOR (FGF23) AND METHODS FOR USE
FILE REFERENCE: 053884-5001
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CURRENT FILING DATE: 2001-07-10
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                                                                                                     ENGYDYYHSPQYHFLVSLGRAKRAFLPGMNPPPYSQFLSRRNEIPLIHFNTPIPRRHTRS 180
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                           AEDDSERDPLNVLKPRARMTPAPASCSQELPSAEDNSPMASDPLGVVRGGRVNTHAGGTG
                                                                               ENGYDVYHSPQYHFLVSLGRAKRAFLPGMNPPPYSQFLSRRNEIPLIHFNTPIPRRHTRS
                                                                                                                                                               VDGAPHQTIYSALMIRSEDAGFVVITGVMSRRYLCMDFRGNIFGSHYFDPENCRFQHQTL 120
AEDDSERDPLNVLKPRARMTPAPASCSQELPSAEDNSPMASDPLGVVRGGRVNTHAGGTG 240
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PRIOR FILING DATE: 1997-06-16
PRIOR APPLICATION NUMBER: 60/062250
PRIOR FILING DATE: 1997-10-17
PRIOR APPLICATION NUMBER: 60/065186
PRIOR FILING DATE: 1997-11-13
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CURRENT FILING DATE: 2001-11-14
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TITLE OF INVENTION: Secreted and Transmembrane Polypeptides and Nucleic
TITLE OF INVENTION: Acids Encoding the Same
FILE REFERENCE: P2730P1C20
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APPLICANT: Baker,Kevin P.
APPLICANT: Botstein,David
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                                                                        DR FILING DATE: 1998-06-02

PR APPLICATION NUMBER: 60/087609

DR FILING DATE: 1998-06-02

DR FILING DATE: 1998-06-02

DR APPLICATION NUMBER: 60/087759

DR FILING DATE: 1998-06-03

DR FILING DATE: 1998-06-03
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FILING DATE: 1997-11-24
APPLICATION NUMBER: 60/075945
FILING DATE: 1998-02-25
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APPLICATION NUMBER: 60/087106
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APPLICATION NUMBER: 60/083322
FILING DATE: 1998-04-28
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FILING DATE
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FILING DATE: 1998-06-04
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FILING DATE: 1998-05-07
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Roy, Margaret Ann
Stewart, Timothy A.
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Gerber, Hanspeter
Gerritsen, Mary E.
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Godowski, Paul J.
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FILING DATE: 1998-06-25
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APPLICATION NUMBER:
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                                                         NUMBER: 60/091978: 1998-07-07
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PRIOR PRIOR PRIOR

APPLICATION NUMBER: 60/088212

1998-06-05

NUMBER: 60/088217

1998-06-05

APPLICATION NUMBER: FILING DATE:

60/088202

APPLICATION NUMBER: 60/088167 APPLICATION NUMBER: 60/088326 FILING DATE: 1998-06-04

1998-06-

FILING DATE:

APPLICATION NUMBER: 60/088655 FILING DATE: 1998-06-05

NUMBER:

60/088734

1998-06-09

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NUMBER: 60/088030 NUMBER: 60/088029

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APPLICATION

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60/088026

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NUMBER: 60/088025 NUMBER: 60/08802: NUMBER: 60/087827

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FILING DATE:

APPLICATION NUMBER: 60/089105

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APPLICATION NUMBER: 60/088858

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APPLICATION NUMBER: 60/088810 FILING DATE: 1998-06-10

APPLICATION NUMBER: 60/088824

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APPLICATION NUMBER: 60/088742

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NUMBER: 60/089907

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60/089908

FILING DATE:

1998-06-18

60/089801 60/089653 60/089600 60/089599 60/089598 60/089538 60/089532 60/089514 60/089512 60/089440

CURRENT APPLICATION NUMBER: US/09/989,735 CURRENT FILING DATE: 2001-11-19 PRIOR APPLICATION NUMBER: 60/049787 PRIOR FILING DATE: 1997-06-16 PRIOR FILING DATE: 1997-10-17 PRIOR APPLICATION NUMBER: 60/062250 PRIOR APPLICATION NUMBER: 60/065186 PRIOR APPLICATION NUMBER: 60/065186 PRIOR APPLICATION NUMBER: 60/06511 PRIOR APPLICATION NUMBER: 60/065311 PRIOR APPLICATION NUMBER: 60/06670 PRIOR APPLICATION NUMBER: 60/06670 PRIOR APPLICATION NUMBER: 60/075945 PRIOR APPLICATION NUMBER: 60/075945 PRIOR APPLICATION NUMBER: 60/078910 PRIOR APPLICATION NUMBER: 60/078910	400004444444444444444444444	Best Local Similarity 100.0%; Pred. No. 2.1e-123; Matches 251; Conservative 0; Mismatches 0; Indels 0; Gaps 0; Qy 1 MIGARLRIMVCALCSVCSMSVLRAYPNASPLIGSSWGGLIHLYTATARNSYHLQIHKNGH 60 Db 1 MIGARLRIMVCALCSVCSMSVLRAYPNASPLIGSSWGGLIHLYTATARNSYHLQIHKNGH 60 QY 61 VDGAPHQTIYSALMIRSEDAGFVVITGVMSRRYLCMDFRGNIFGSHYFDDENCREQHQTL 120 Db 61 VDGAPHQTIYSALMIRSEDAGFVVITGVMSRRYLCMDFRGNIFGSHYFDDENCREQHQTL 120 QY 121 ENGYDVYHSPQYHFLVSLGRAKRAFLPGMNPPPYSQFLSRRNEIPLHFNTPIPRRHTRS 180 Db 121 ENGYDVYHSPQYHFLVSLGRAKRAFLPGMNPPPYSQFLSRRNEIPLHFNTPIPRRHTRS 180 QY 181 AEDDSERDPLNVLKERARMTPAPASCSQELPSAEDNSPMASDPLGVVRGGRVNTHAGGTG 240 QY 181 AEDDSERDPLNVLKERARMTPAPASCSQELPSAEDNSPMASDPLGVVRGGRVNTHAGGTG 240 QY 241 PEGCRPFAKFI 251 Db 241 YBGCRPFAKFI 251
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APPLICATION NUMBER:

APPLICATION NUMBER: 60/089952 FILING DATE: 1998-06-1

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60/090246

NUMBER: 60/089948

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60/089947 60/089908 60/089907 60/089801 60/089653 60/089600

FILING DATE: FILING DATE:

1998-06-22

APPLICATION NUMBER: 60/090355

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Matches 251
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CURRENT APPLICATION NUMBER: US/09/990,444
CURRENT FILING DATE: 2001-11-14
PRIOR APPLICATION NUMBER: 60/049787
PRIOR FILING DATE: 1997-06-16
PRIOR APPLICATION NUMBER: 60/062250
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TITLE OF INVENTION: Secreted and Transmembrane Polypeptides
TITLE OF INVENTION: Acids Encoding the Same
FILE REFERENCE: P2730P1C19
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DR APPLICATION NUMBER: 60/091978

DR FILING DATE: 1998-07-07

DR APPLICATION NUMBER: 60/091982

DR FILING DATE: 1998-07-07

DR APPLICATION NUMBER: 60/092182

DR FILING DATE: 1998-07-09

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Wood, William I.
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Kljavin, Ivar J
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Botstein, David
                                                                                                                                                                                                                                                                                                                                              Godowski, Paul
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Pred. No. 2.1e-123;
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PRIOR PRIOR

APPLICATION NUMBER: 60/090694 FILING DATE: 1998-06-25

FILING DATE: FILING DATE:

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APPLICATION NUMBER:

60/090690

APPLICATION NUMBER:

60/090678

APPLICATION NUMBER: 60/090676

1998-06-24

60/090557

APPLICATION NUMBER: FILING DATE:

FILING DATE:

APPLICATION NUMBER: 60/090542

1998-06-24

1998-06-24

FILING DATE:

APPLICATION NUMBER: 60/090540

1998-06-24

APPLICATION NUMBER:

60/090472

APPLICATION NUMBER:

1998-06-24

60/090535

APPLICATION NUMBER: 60/090445 APPLICATION NUMBER: 60/090444 FILING DATE: 1998-06-24

1998-06-24 1998-06-24 1998-06-24 1998-06-24

APPLICATION NUMBER: FILING DATE:

60/090435

APPLICATION NUMBER: 60/090431

FILING DATE: FILING DATE: FILING DATE: FILING DATE:

APPLICATION

NUMBER: 60/090429

1998-06-23

1998-06-24

APPLICATION FILING DATE:

FILING DATE:

NUMBER: 60/090696 NUMBER: 60/090695

1998-06-25

1998-06-25

APPLICATION NUMBER: 60/091544
FILING DATE: 1998-07-01
APPLICATION NUMBER: 60/091519
FILING DATE: 1998-07-02

NUMBER: 60/091626: 1998-07-02

60/091633

APPLICATION NUMBER: 60/091478

1998-07-

FILING DATE:

APPLICATION FILING DATE:

NUMBER:

60/091360

1998-07-01 1998-06-26 APPLICATION NUMBER:

60/090863

FILING DATE:

APPLICATION NUMBER: 60/090862 FILING DATE: 1998-06-26

60/065311

PRIOR OR FILING DATE: 1998-06-24
OR APPLICATION NUMBER: 60/090540
OR APPLICATION NUMBER: 60/090542
OR APPLICATION NUMBER: 60/090542
OR FILING DATE: 1998-06-24
OR FILING DATE: 1998-06-24
OR APPLICATION NUMBER: 60/09057
OR FILING DATE: 1998-06-25
OR APPLICATION NUMBER: 60/090676
OR FILING DATE: 1998-06-25
OR APPLICATION NUMBER: 60/090678
OR APPLICATION NUMBER: 60/090690
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OR APPLICATION NUMBER: 60/090695 OR APPLICATION NUMBER: 60/090431
OR FILING DATE: 1998-06-24
OR APPLICATION NUMBER: 60/090435
OR PILING DATE: 1998-06-24
OR APPLICATION NUMBER: 60/090444
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OR APPLICATION NUMBER: 60/090445
OR APPLICATION NUMBER: 60/090472
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FILING DATE: 1998-06-23
APPLICATION NUMBER: 60/090429 FILING DATE: 1998-06 APPLICATION NUMBER: FILING DATE: 1998-06-19 APPLICATION NUMBER: 60/090246 APPLICATION NUMBER: FILING DATE: 1998-06-19 APPLICATION NUMBER: 60/089948 FILING DATE: 1998-06-18 APPLICATION NUMBER: 60/089947 APPLICATION NUMBER: 60 FILING DATE: 1998-06-1 FILING DATE: 1998-06-18
APPLICATION NUMBER: 60/089908 FILING DATE: 1998-0 APPLICATION NUMBER: FILING DATE: FILING DATE: 1998-06-17 APPLICATION NUMBER: 60/089653 APPLICATION NUMBER: FILING DATE: 1998-0 APPLICATION NUMBER: APPLICATION NUMBER: APPLICATION NUMBER: 60 FILING DATE: 1998-06-1 FILING LING DATE: LING DATE: LING DATE: DATE: NUMBER: 60/089532 1998-06-24 1998-06-1998-06-22 1998-06-22 1998-06-19 1998-06-22 1998-06-1998-06-16 1998-06-18 1998-06-17 1998-06-60/091360 60/090862 60/090696 60/090863 60/090349 60/090254 60/090252 60/08980 60/089952 60/089907 60/089600 60/089599 60/089598 60/089538

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APPLICATION NUMBER: 60/088876 FILING DATE: 1998-06-11 FILING DATE: 1998-06-10 APPLICATION NUMBER: FILING DATE: APPLICATION NUMBER: FILING DATE: APPLICATION NUMBER: 60/088734 APPLICATION NUMBER: 60/088655 FILING DATE: 1998-06-09 FILING DATE: APPLICATION NUMBER: FILING DATE: APPLICATION 1 APPLICATION FILING DATE: APPLICATION FILING DATE: 1998-06 APPLICATION NUMBER: FILING DATE: 1998-00 APPLICATION NUMBER: PILING DATE: 1998-06 APPLICATION NUMBER: APPLICATION NUMBER: 60/088021 APPLICATION NUMBER: FILING DATE: 1998-06-02 APPLICATION NUMBER: 60/087759 APPLICATION APPLICATION : FILING DATE: APPLICATION NUMBER: 60/078910 FILING DATE: 1998-03-20 APPLICATION NUMBER: 60/075945 FILING DATE: 1998-02-25 APPLICATION APPLICATION NUMBER: 60/088033 FILING DATE: APPLICATION NUMBER: APPLICATION FILING DATE: FILING DATE: FILING DATE: APPLICATION NUMBER: 60/087609 FILING DATE: APPLICATION NUMBER: FILING DATE: APPLICATION FILING DATE: FILING DATE: LING DATE: NUMBER: 60/089512 : 1998-06-16 NUMBER: NUMBER: NUMBER: 60/088861 NUMBER: 60/088202 NUMBER: NUMBER: NUMBER: 60/088026 NUMBER: NUMBER: 60: 1997-11-1 NUMBER: 60/084600: 1998-05-07 NUMBER: 60/083322 NUMBER: 60/066770 1998-06-11 1998-06-16 1998-06-12 1998-06-10 1998-06-10 1998-06-05 1998-06-05 1998-06-05 1998-06-05 1998-06-04 1998-06-1998-06-04 1998-06-04 1998-06-04 1998-06-04 1998-06-04 1998-06-02 1998-06-02 1998-04-1998-06-04 1998-06-03 1998-05-60/089440 60/088826 60/088738 60/089514 60/089105 60/088742 60/088217 60/088212 60/088167 60/088326 60/088030 60/088029 60/088025 60/088028 60/087827 60/087607 60/087106

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RESULT 6
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APPLICANT: Baker, Kevin P.
APPLICANT: Botstein, David
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FILING DATE: 1998-07-02
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FILING DATE: 1998-07-07
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               INVENTION:
                                        Tumas, Daniel
Watanabe, Colin K.
Williams, P. Mickey
Wood, William I.
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Gerritsen, Mary E.
Goddard, Audrey
                                                                                                 Paoni, Nicholas F.
Roy, Margaret Ann
Stewart, Timothy A.
                                                                                                                                                                         Grimaldi, J.Christopher Gurney, Austin L. Kljavin, Ivar J.
                                                                                                                                                          Napier, Mary A.
                                                                                                                                                                                                                     Godowski, Paul J.
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Pred. No. 2.1e-123;
; Mismatches 0;
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FILE REFERENCE: P2730P1C69
CURRENT APPLICATION NUMBER: US/09/989,730
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FILING DATE: 1998-06-09
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                                                                        FILING DATE: 1998-06 APPLICATION NUMBER:
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NUMBER:

60/089109 60/088876

1998-06-12 1998-06-16

NUMBER:

FILING DATE: 1998-06-16

NUMBER:

60/089512

NUMBER: 60/089440

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RESULT 7
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; Sequence No. US20020198148A1
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APPLICATION NUMBER: 6
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FILING DATE: 1998-07-01
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APPLICATION NUMBER: 60/090696
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                                                                                   Fong, Sherman
Gerber, Hanspeter
Gerritsen, Mary E.
Goddard, Audrey
Godowski, Paul J.
Grimaldi, J. Christopher
Gurney, Austin L.
Kljavin, Ivar J.
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Baker, Kevin P.
Paoni, Nicholas F.
                                                      Napier, Mary A.
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APPLICATION NUMBER: 60/090540 FILING DATE: 1998-06-24

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NUMBER:

60/090535 60/090472 60/090445

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APPLICATION NUMBER: 60/090444 FILING DATE: 1998-06-24

FILING DATE: 1998-06-24 APPLICATION NUMBER: 60/090435

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APPLICATION NUMBER: 60/090355

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APPLICATION NUMBER: 60/090246

APPLICATION NUMBER: 60/089952 FILING DATE: 1998-06-19 APPLICATION NUMBER:

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APPLICATION NUMBER: 60/089947 APPLICATION NUMBER: 60/089908

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FILING DATE: 1998-06-18

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APPLICATION NUMBER: 60/089907

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60/089598 60/089536

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FILING DATE: 1998-06-16 APPLICATION NUMBER: 60/089532 APPLICATION NUMBER: 60/089514

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PRIOR APPLICATION NUMBER: 60/
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PPLICANT: Zhang, Zemin
ITLE OF INVENTION: Secreted and
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ILE REFERENCE: P2730P1C14
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APPLICATION NUMBER: 60/066770
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FILING DATE: 1998-06-05
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FILING DATE: 1998-06-02
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Stewart, Timothy A.
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FILING DATE: 1998-06-24
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FILING DATE: 1998-06-22
APPLICATION NUMBER: 60/090349
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APPLICATION NUMBER: 60/090252
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FILING DATE: 1998-06-18
APPLICATION NUMBER: 60/089907
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APPLICATION NUMBER: 60/089512
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APPLICATION NUMBER: 60/089440
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APPLICATION NUMBER: 60/088824
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APPLICATION 1
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FILING DATE: 1998-06-24
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APPLICATION NUMBER: 60/090429
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APPLICATION NUMBER: 60/090355
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Best Local Sim
Matches 251;
          APPLICANT: Ashkenazi, Avi J.
APPLICANT: Baker, Kevin P.
APPLICANT: Botstein, David
APPLICANT: Desnoyers, Luc
APPLICANT: Eaton, Dan L.
APPLICANT: Ferrara, Napoleone
APPLICANT: Fong, Sherman
                                                                                                                            Sequence 511, Application US/09991181 Publication No. US20020197615A1
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APPLICATION NUMBER: 60/092182
FILING DATE: 1998-07-09
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Pred. No. 2.1e-123;
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PRIOR FILING DATE: 1997-06-16
PRIOR APPLICATION NUMBER: 60/062250
PRIOR FILING DATE: 1997-10-17
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R FILING DATE: 1998-06-
R APPLICATION NUMBER: 6
R FILING DATE: 1998-06-
APPLICATION NUMBER: 60/088202
FILING DATE: 1998-06-05
APPLICATION NUMBER: 60/088212
FILING DATE: 1998-06-05
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APPLICATION NUMBER: 60/088028
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FILING DATE: 1998-06-04
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APPLICATION NUMBER: 60/087759
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APPLICATION NUMBER: 60/087607
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Goddard, Audrey
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Williams, P. Mickey
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Kljavin, Ivar J.
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Grimaldi, J.Christopher
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Stewart, Timothy A.
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FILING DATE: 1998-06-16
APPLICATION NUMBER: 60/089512
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                  PEGCRPFAKFI
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PEGCRPFAKFI
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WS-09-93-687-511 US-09-93-687-511 ; Sequence 511, Application US/09993687 ; Publication No. US20020198149A1

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FILLING DATE: 1998-06-23
APPLICATION NUMBER: 60/090429
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FILING DATE: 1998-06-23 APPLICATION NUMBER: 60/090355

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APPLICATION NUMBER: 60/090252
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APPLICATION NUMBER: 60/089908
FILING DATE: 1998-06-18

FILING DATE: 1998-06-17
APPLICATION NUMBER: 60/089801
FILING DATE: 1998-06-18
APPLICATION NUMBER: 60/089907

FILING DATE: 1998-06-17 APPLICATION NUMBER: 60/089653 APPLICATION NUMBER: 60/089600 FILING DATE: 1998-06 APPLICATION NUMBER:

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FILING DATE: 1998-06-16 APPLICATION NUMBER: 60/089532

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CURRENT APPLICATION NUMBER: US/09/993,687
CURRENT FILING DATE: 2002-11-14
PRIOR APPLICATION NUMBER: 60/049787
PRIOR FILING DATE: 1997-06-16
PRIOR APPLICATION NUMBER: 60/062250
PRIOR FILLING DATE: 1997-10-17
PRIOR APPLICATION NUMBER: 60/065186
PRIOR FILLING DATE: 1997-11-12
PRIOR APPLICATION NUMBER: 60/065311
PRIOR FILLING DATE: 1997-11-13
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PRIOR APPLICATION NUMBER: 60/066770
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: Baker,Kevin P.
: Botstein,David
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Roy, Margaret Ann
Stewart, Timothy A.
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Gerber, Hanspeter
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Grimaldi,J.Christopher
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APPLICATION NUMBER: 60/088021
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Stewart, Timothy A.
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Williams, P. Mickey
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APPLICATION NUMBER: 60/090444
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VDGAPHOTIYSALMIRSEDAGFVVITGVMSRRYLCMDFRGNIFGSHYFDPENCRFQHOTL 120
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APPLICATION NUMBER: 60/088810 FILING DATE: 1998-06-10

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APPLICATION NUMBER: 60/088876

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APPLICATION NUMBER: 60/088826 FILING DATE: 1998-06-10 APPLICATION NUMBER: 60/088824

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APPLICATION NUMBER: 60/088655 FILING DATE: 1998-06-09 APPLICATION NUMBER: 60/088734

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APPLICATION NUMBER: 60/089653 FILING DATE: 1998-06-17 APPLICATION NUMBER: 60/089801

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Publication No.
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FILE REFERENCE:
CURRENT APPLICATION NUMBER: US/10/028,072
CURRENT FILING DATE: 2001-12-19
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Gurney, Austin L.
Sherwood, Steven
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Filvaroff, Ellen
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APPLICATION NUMBER: 60/081203
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APPLICATION NUMBER: 60/079728
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APPLICATION NUMBER: 60/078910
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APPLICATION NUMBER: 60/079294
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APPLICATION NUMBER: 60/074092
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APPLICATION NUMBER: 60/074086
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Query Match
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US-09-997-653-511 VS-09-997-653-511 ; Sequence 511, Application US/09997653 publication No. US20030008297A1 CURRENT FILING DATE: 127304103

CURRENT FILING DATE: 2001-11-15

PRIOR APPLICATION NUMBER: 60/049787

PRIOR PELING DATE: 1997-06-16

PRIOR APPLICATION NUMBER: 60/062250

PRIOR APPLICATION NUMBER: 60/062250

PRIOR APPLICATION NUMBER: 60/065186

PRIOR PILING DATE: 1997-11-12

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PRIOR FILLING DATE: 1998-06-17 PRIOR APPLICATION NUMBER: 60/089653 PRIOR FILLING DATE: 1998-06-18 PRIOR PELLING DATE: 1998-06-18 PRIOR APPLICATION NUMBER: 60/089908 PRIOR APPLICATION NUMBER: 60/089908 PRIOR FILLING DATE: 1998-06-19 PRIOR APPLICATION NUMBER: 60/089908 PRIOR APPLICATION NUMBER: 60/089908 PRIOR APPLICATION NUMBER: 60/08994 PRIOR APPLICATION NUMBER: 60/08994 PRIOR APPLICATION NUMBER: 60/08994 PRIOR PILLING DATE: 1998-06-19 PRIOR APPLICATION NUMBER: 60/090252 PRIOR PILLING DATE: 1998-06-29 PRIOR APPLICATION NUMBER: 60/090252 PRIOR PILLING DATE: 1998-06-29 PRIOR APPLICATION NUMBER: 60/090254 PRIOR APPLICATION NUMBER: 60/090355 PRIOR APPLICATION NUMBER: 60/090359 PRIOR PILLING DATE: 1998-06-23 PRIOR APPLICATION NUMBER: 60/090431 PRIOR APPLICATION NUMBER: 60/090444 PRIOR APPLICATION NUMBER: 60/090445 PRIOR APPLICATION NUMBER: 60/090445 PRIOR APPLICATION NUMBER: 60/090445 PRIOR APPLICATION NUMBER: 60/090445 PRIOR APPLICATION NUMBER: 60/090540 PRIOR PILLING DATE: 1998-06-24 PRIOR APPLICATION NUMBER: 60/090540 PRIOR PILLING DATE: 1998-06-24 PRIOR APPLICATION NUMBER: 60/090540 PRIOR PILLING DATE: 1998-06-24 PRIOR APPLICATION NUMBER: 60/090540 PRIOR PILLING DATE: 1998-06-25 PRIOR APPLICATION NUMBER: 60/090540 PRIOR PILLING DATE: 1998-06-25 PRIOR APPLICATION NUMBER: 60/090540 PRIOR PILLING DATE: 1998-06-25 PRIOR PILLING DATE: 1998-06-25 PRIOR APPLICATION NUMBER: 60/09069 PRIOR PILLING DATE: 1998-06-25 PRIOR PILLING DATE: 1998-06-25 PRIOR APPLICATION NUMBER: 60/09069 PRIOR PILLING DATE: 1998-06-25 PRIOR PILLING DATE: 1998-06-26 PRIOR PILLING DATE: 1998-06-26 PRIOR PILLING DATE: 1998-07-01 PRIOR APPLICATION NUMBER: 60/090862 PRIOR PILLING DATE: 1998-07-01 PRIOR PILLING DATE: 1			
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FILING DATE: 1998-06-09
APPLICATION NUMBER: 60/088734
FILING DATE: 1998-06-10

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FILING DATE: 1998-06-05 APPLICATION NUMBER: 60/ FILING DATE: 1998-06-05

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FILING DATE: 1998-06-04
APPLICATION NUMBER: 60/088167
FILING DATE: 1998-06-05

FILING DATE: 1998-06-04 APPLICATION NUMBER: 60/088326 FILING DATE: 1998-06-04
APPLICATION NUMBER: 60/088033 APPLICATION NUMBER: 60/088030 APPLICATION NUMBER: 60/088026 FILING DATE: 1998-06-04 APPLICATION NUMBER: 60/088028

FILING DATE: 1998-06-04

APPLICATION

NUMBER: 60/088025 NUMBER: 60/088021 NUMBER: 60/087827 NUMBER: 60/087759 NUMBER: 60/087609 NUMBER: 60/087607

FILING DATE: 1998-06-04 APPLICATION NUMBER: 60/088029

ILING DATE: 1998-06-04

APPLICATION NUMBER: 60/0 FILING DATE: 1998-06-02 APPLICATION NUMBER: 60/0 FILING DATE: 1998-06-03

APPLICATION NUMBER: 60/ FILING DATE: 1998-06-04

FILING DATE: 1998-06-02 FILING DATE: 1998-06-02 APPLICATION NUMBER: 60/

DATE: 1998-05-28

NUMBER:

60/087106

NUMBER: 60/084600 : 1998-05-07

PRIOR PRIOR PRIOR PRIOR

FILING DATE: 1998-00 APPLICATION NUMBER:

1998-06-11

60/088876

APPLICATION NUMBER: 60/088861

FILING DATE: 1998-06-10 APPLICATION NUMBER: 60/088858 FILING DATE: 1998-06-11

APPLICATION NUMBER: 60/088824 FILING DATE: 1998-06-10 APPLICATION NUMBER: 60/088826

APPLICATION NUMBER: 60/088742 FILING DATE: 1998-06-10 APPLICATION NUMBER: 60/088810 FILING DATE: 1998-06-10

PRIOR PRIOR

FILLING DATE: 1998-06-12
APPLICATION NUMBER: 60/089440
FILING DATE: 1998-06-16
APPLICATION NUMBER: 60/089512 FILING DATE: 1998-06-11
APPLICATION NUMBER: 60/089105
FILING DATE: 1998-06-12

OR FILING DATE: 1998-06-16
OR APPLICATION NUMBER: 60/089514
OR FILING DATE: 1998-06-16
OR APPLICATION NUMBER: 60/089532
OR FILING DATE: 1998-06-17
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            CURRENT APPLICATION NUMBER: US/09/993,667
CURRENT FILING DATE: 2001-11-14
PRIOR APPLICATION NUMBER: 60/049787
PRIOR FILING DATE: 1997-06-16
PRIOR APPLICATION NUMBER: 60/062250
PRIOR FILING DATE: 1997-10-17
PRIOR APPLICATION NUMBER: 60/065186
PRIOR APPLICATION NUMBER: 60/065186
PRIOR FILING DATE: 1997-11-12
PRIOR FILING DATE: 1997-11-12
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Best Local Simi
Matches 251;
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                                                                                                                                             TITLE OF INVENTION: Secreted and Transmembrane Polypeptides and Nucleic TITLE OF INVENTION: Acids Encoding the Same FILE REFERENCE: P2730P1C4
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         APPLICANT: Ashkenazi,Avi J.
APPLICANT: Baker,Kevin P.
APPLICANT: Botstein,David
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R FILING DATE: 1998-07-07

OR APPLICATION NUMBER: 60/091982

R FILING DATE: 1998-07-07

OR APPLICATION NUMBER: 60/092182

OR FILING DATE: 1998-07-09
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                                                                                                                                                                                                                                                                          Paon, Nicholas F.
Roy, Margaret Ann
Stewart, Timothy A.
                                                                                                                                                                                                   Zhang, Zemin
                                                                                                                                                                                                             Watanabe, Colin K. Williams, P. Mickey Wood, William I.
                                                                                                                                                                                                                                                                   Tumas,
                                                                                                                                                                                                                                                                                                                                                                  Gurney, Austin L. Kljavin, Ivar J.
                                                                                                                                                                                                                                                                                                                                                                                                   Godowski, Paul J.
Grimaldi, J. Christopher
                                                                                                                                                                                                                                                                                                                                                                                                                                     Goddard, Audrey
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Gerber, Hanspeter
                                                                                                                                                                                                                                                                                                                                                  Napier, Mary A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Ferrara, Napoleone
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Fong, Sherman
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o. US20030022187A1
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                                                                                                                                                                                                                                                                                                                                        , James
                                                                                                                                                                                                                                                              Daniel
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60/065311
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Pred. No. 2.1e-123;
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PRIOR OR FILING DATE: 1998-06-11
OR APPLICATION NUMBER: 60/089105
OR FILING DATE: 1998-06-12
OR APPLICATION NUMBER: 60/089440
OR FILING DATE: 1998-06-16
OR APPLICATION NUMBER: 60/089512
OR FILING DATE: 1998-06-16
OR APPLICATION NUMBER: 60/089514 APPLICATION NUMBER: 60/088861 FILING DATE: 1998-06-11 APPLICATION NUMBER: 60/088876 APPLICATION NUMBER: 60/088826 FILING DATE: 1998-06-10 APPLICATION NUMBER: 60/088858 APPLICATION NUMBER: 60/088810 FILING DATE: 1998-06-10 APPLICATION NUMBER: 60/088824 FILING DATE: 1998-06-10 APPLICATION NUMBER: 60/088738 FILING DATE: 1998-06-10 APPLICATION NUMBER: 60/088742 FILING DATE: APPLICATION NUMBER: APPLICATION NUMBER: 60/088655 APPLICATION NUMBER: 60/088217 APPLICATION NUMBER: 60/088033 FILING DATE: 1998-06-04 APPLICATION NUMBER: 60/088326 APPLICATION NUMBER: 60/088212 FILING DATE: 1998-06-05 APPLICATION NUMBER: 60/088202 APPLICATION NUMBER: FILING DATE: 1998-06 APPLICATION NUMBER: APPLICATION NUMBER: FILING DATE: 1998-0 APPLICATION NUMBER: APPLICATION NUMBER: APPLICATION NUMBER: 60/088021 APPLICATION NUMBER: 60/087607 FILING DATE: 1998-06-02 FILING DATE: APPLICATION NUMBER: 60/078910 APPLICATION NUMBER: FILING DATE: APPLICATION NUMBER: APPLICATION NUMBER: 60/083322 FILING DATE: APPLICATION NUMBER: 60/066770 FILING DATE: APPLICATION NUMBER: FILING DATE: 1998-05 APPLICATION NUMBER: 60/075945 PPLICATION NUMBER: PPLICATION NUMBER: LING DATE: LING DATE LING DATE: 1998-06-05 LING DATE: LING DATE: 1998-06-LING DATE: LING DATE: LING DATE: ING DATE: ING DATE: LING DATE: 1998-06-02 LING DATE: 1997-11-24 1998-06-1 1998-06-10 1998-06-05 1998-06-10 1998-06-05 1998-06-09 1998-06-05 1998-06-03 1997-11-13 1998-06-04 1998-06-04 1998-06-04 1998-06-04 1998-06-02 1998-06-02 1998-05-28 1998-05-07 1998-04-28 1998-03-1998-06-04 1998-06-04 1998-02-60/088734 60/088167 60/088028 60/088029 60/088026 60/088030 60/088025 60/087827 60/087759 60/087609 60/087106 60/084600

PRIOR

FILING DATE: 1998-06-18

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NUMBER:

60/089653

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NUMBER: 60/089599

1998-06-17 1998-06-1 APPLICATION NUMBER:

60/089598 60/089538

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1998-06-18 1998-06-17 1998-06-17

APPLICATION N

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NUMBER: 60/089947 NUMBER: 60/089908 NUMBER: 60/089907 NUMBER: 60/089801

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1998-06-18

PRIOR

APPLICATION NUMBER: FILING DATE: 1998-07-02

60/091544

FILING DATE: 1998-07-01

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RESULT 14
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NUMBER OF SEQ
SEQ ID NO 266
LENGTH: 251
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Matches 251
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Publication No
                                                                                                                                                                                                                                                                                                                                                                                               GENERAL
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                                                              APPLICANT: Zhang, Zemin
TITLE OF INVENTION: SECRETED AND TRANSMEMBRANE
TITLE OF INVENTION: ACIDS ENCODING THE SAME
FILE REFERENCE: 93330R1C17
CURRENT APPLICATION NUMBER: US/10/121,049
CURRENT FILING DATE: 2002-04-12
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                                    Prior Application 3R OF SEQ ID NOS: 5
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FILING DATE: 1998-07-02
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APPLICATION NUMBER: 60/0
FILING DATE: 1998-07-07
APPLICATION NUMBER: 60/0
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FILING DATE: 1998-07-02
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                                                                                                                                                                                                                                                                                                                                                                                                               No.
                                                                                                                                                                                                                                                                                                                   DeForge, Laura
Desnoyers, Luc
Filvaroff, Ellen
                                                                                                                                                                                                                                                                                                                                                                                Baker, Kevin P.
                                                                                                                                                                                                                             Godowski, Paul J.
Gurney, Austin L.
Sherwood, Steven
                                                                                                                                                      Wood, William
                                                                                                                                                                                                                                                                                        Gao, Wei-Qiang
Gerritsen, Mary E
                                                                                                                                                                       Watanabe, Colin K
                                                                                                                                                                                                 Stewart, Timothy A.
                                                                                                                                                                                                                                                                                                                                                                 Beresini, Maureen
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o. US20030022239A1
                                                                                                                                                                                     Tumas,Daniel
                                                                                                                                                                                                                  Smith, Victoria
                                                                                                                                                                                                                                                                           Goddard, Audrey
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Pred. No. 2.1e-123;
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PRIOR

APPLICATION I FILING DATE: APPLICATION

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NUMBER: NUMBER:

60/090444 60/090439

1998-06-24

PLICATION

NUMBER: 60/090472 NUMBER: 60/090445

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NUMBER: 60/090540

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FILING DATE: 1998-06-24 APPLICATION NUMBER: 60/090431

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APPLICATION NUMBER: 60/090252

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APPLICATION FILING DATE: FILING DATE:

NUMBER:

60/090678 60/090676

APPLICATION NUMBER:

APPLICATION

NUMBER: 60/090557

1998-06-24

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APPLICATION NUMBER: FILING DATE: 1998-06

APPLICATION NUMBER: FILING DATE: 1998-06

NUMBER: 60/091360

1998-06-26 1998-06-26 1998-06-25

60/090863

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APPLICANT: Zhang, Zemin
TITLE OF INVENTION: SECRETED AND TRANSMEMBRANE POLYPEPTIDES AND NUCLEIC
TITLE OF INVENTION: ACIDS ENCODING THE SAME
FILE REFERENCE: P3330R1C54
CURRENT APPLICATION NUMBER: US/10/123,904
CURRENT FILING DATE: 2002-04-16
Prior Application removed - See File Wrapper or Palm
NUMBER OF SEQ ID NOS: 550
SEQ ID NO 266
LENGTH: 251
TYPE: PRT
ORGANISM: Homo Sapien
US-10-123-904-266
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                                                                                                                       Query Match
Best Local Similarity
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Sequence 266, Application US/10123904
Publication No. US20030022328A1
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Watanabe, Colin K
Wood, William
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Gurney, Austin L.
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                                                                                                                     100.0%; Silarity 100.0%; For Conservative 0;
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Pred. No. 2.1e-123;
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                                                       AEDDSERDPLNVLKPRARMTPAPASCSQELPSAEDNSPMASDPLGVVRGGRVNTHAGGTG 240
                                                                          AEDDSERDPLNVLKPRARMTPAPASCSQELPSAEDNSPMASDPLGVVRGGRVNTHAGGTG 240
                           PEGCRPFAKFI 251
                                                                                                                      ENGYDVYHSPQYHFLVSLGRAKRAFLPGMNPPPYSQFLSRRNEIPLIHFNTPIPRRHTRS 180
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Search completed: May 23, 2003, 07:58:43 Job time: 736 secs

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Result
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Maximum DB seq length: 2000000000
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1: /cgn2_6/ptodata/1/laa/5A_COMB.pep:*

2: /cgn2_6/ptodata/1/laa/5B_COMB.pep:*

3: /cgn2_6/ptodata/1/laa/6A_COMB.pep:*

4: /cgn2_6/ptodata/1/laa/6B_COMB.pep:*

5: /cgn2_6/ptodata/1/laa/PCTUS_COMB.pep:*

6: /cgn2_6/ptodata/1/laa/backfiles1.pep:*
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Sequence 14, Appl
Sequence 15, Appl
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153.5	153.5	153.5	154	154	156	162	167.5	168.5	168.5	168.5	168.5	168.5	168.5	168.5	168.5	168.5	168.5
11.3	11.3	11.3	11.3	11.3	11.5	11.9	12.3	12.4	12.4	12.4	12.4	12.4	12.4	12.4	12.4	12.4	12.4
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_				Sequence 18,	Patent No. 51			ω ω	'n		Sequence 15,			ω,	Sequence 12,	Sequence 12,	Sequence 17,
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AL I GNMENTS

US-08-439-725A-11

Sequence 11, Application US/08439725A
PATENT NO. 5693775
GENERAL INFORMATION:
APPLICANT: Nathans, Jeremy
APPLICANT: Smallwood, Philip M.
APPLICANT: Macke, Jennifer P.
APPLICANT: Macke, Jennifer P.
TITLE OF INVENTION: FIBROBROBLAST GROWTH FACTOR HOMOLOGOUS
TITLE OF INVENTION: FACTOR-1 (FHF-1) AND METHODS OF USE

NUMBER OF SEQUENCES: 1

STREET: 4225 EXCITY: La Jolla STATE: CA

USA

ADDRESSEE: Fish & Richardson P.C. STREET: 4225 Executive Square, Suite 1400

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                                                                                                                                               US-08-439-725A-11
                                                                      Best Local Similarity
Matches 63; Conser
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INFORMATION FOR SEQ ID NO:
SEQUENCE CHARACTERISTICS:
                                                                                                                                                           STRANDEDNESS:
TOPOLOGY: lin
MOLECULE TYPE:
                                                                                                                                                                                                                                                                                   REFERENCE/DOCKET NUMBER: 07
TELECOMMUNICATION INFORMATION:
TELLEPHONE: 619/678-5070
TELEPAX: 617/678-5099
                                                                                                                                                                                                                                                                                                                                                      CLASSIFICATION: 424
ATTORNEY/AGENT INFORMATION:
NAME: Haile, Lisa A.
REGISTRATION NUMBER: 38,
                                                                                                                                                                                                                                                                                                                                                                                                                                                             SOFTWARE: PatentIn Release #1.0, Version #1.30 CURRENT APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IEM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
       48
                                                                                                                                                                                                              TYPE: amino acid
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        COUNTRY: U
ZIP: 92037
                                  42 LYTATARNSYHLQIHKNGHVDGAPHQTIYSALMIRSEDAGFVVITGVMSRRYLCMDFRGN 101
                                                                                                                                                                                                                                                                                                                                                                                                                             APPLICATION NUMBER: US/0 FILING DATE: 12-MAY-1995
                                                                                                                                                                                                                                LENGTH: 245 amino acids
LYCAT---KYHLQLHPSGRVNGSLENSAYSILEITAVEVGVVAIKGLFSGRYLAMNKRGR 104
                                                                          Conservative
                                                                                                                                                                               linear
                                                                                                                                                           protein
                                                                                                                                                                                            not relevant
                                                                                       13.4%; Score 182.5; DB 29.4%; Pred. No. 6.7e-12
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                                                                        Mismatches
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                                                                                                                                                                            Matches
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Best Local :
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GENERAL INFORMATION:
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NFORMATION FOR SEQ ID NO: SEQUENCE CHARACTERISTICS:
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MEDIUM TYPE: Ploppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
                                                                                                                                                                                                                                                                                                                                                                                                                                                              ATTORNEY/AGENT INFORMATION:
NAME: Haile, Lisa A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             CLASSIFICATION: 536
PRIOR APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   SOFTWARE: PatentIn Release #1.0, CURRENT APPLICATION DATA:
                                         105
                                                                                                                                                                                                                                                              MOLECULE TYPE:
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                                                                102 IFGSHYFDPENCRFQHQTLENGYDVYHSPQYHFLVSLGRAKRAFLPGMNPP-----
153 -PYSQFLSRRNEIPLIHFNTPIPR-----RHTRSAEDDSERDPLNVLKPRARMTPAPA 204
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  162 RPRRGFKTRRTQKSSLF--
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                                                                                                                                  42 LYTATARNSYHLQIHKNGHYDGAPHQTIYSALMIRSEDAGFYVVITGVMSRRYLCMDFRGN 101
                                                                                                                                                                                                                                                                                       STRANDEDNESS:
                                                                                                                                                                                                                                                                                                            TYPE: amino acid
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PPLICANT: Macke, Jennifer P.
TILE OF INVENTION: FIBROBROBLAST GROWTH
TILE OF INVENTION: FACTOR-1 (FHF-1) AND
                                                                                                                                                                                                                                                                                TOPOLOGY:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               APPLICATION NUMBER: 08/439,725
FILING DATE: 12-MAY-1995
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                                                                                                                                                                                          Local Similarity
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                               LYASDHYNAB-CEFVERIHELGYNTYASRLYRTGSSGPGAORO--PGAORPWYVSVNGKG 161
                                                                                                   LYCAT---KYHLQLHPSGRVNGSLENSAYSILEITAVEVGVVAIKGLFSGRYLAMNKRGR 104
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                                                                                                                                                                         26;
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                                                                                                                                                                                     Score 182.5; DB 2
Pred. No. 6.7e-12;
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US-08-438-439C-7
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INFORMATION FOR SEQ ID NO:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   ATTORNEY/AGENT INFORMATION:
NAME: Haile, Lisa A.
REGISTRATION NUMBER: 38,
REFERENCE/DOCKET NUMBER:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         COMPUTER READABLE FORM: MEDIUM TYPE: Floppy
                                                                                                                                                                                                                                                                                                                              TOPOLOGY: 1: MOLECULE TYPE:
                                                                                                                                                                                                                                                                                                                                                                                         SEQUENCE CHARACTERISTICS:
LENGTH: 245 amino acid
                                                                                                                                                                                                                                                                                                                                                                                                                                      TELECOMMUNICATION INFORMATION:
TELEPHONE: 619/678-5070
TELEFAX: 619/678-5099
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               CURRENT APPLICATION DATA:
   212
                                 205
                                                                162
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                                                                                                                                                   102 IFGSHYFDPENCRFQHQTLENGYDVYHSPQYHFLVSLGRAKRAFLPGMNPP----- 152
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     TITLE OF INVENTION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  APPLICANT:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     APPLICANT:
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                                                                                                                                                                                                                                                                 Local
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            SOFTWARE: PatentIn Release #1.0,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          COMPUTER: IBM PC OPERATING SYSTEM:
                                                                                                                                                                                                                                                                                                                                                                            HAYPE:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                APPLICATION NUMBER:
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                                                                                                                                                                                LYCAT---KYHLOLHPSGRVNGSLENSAYSILEITAVEVGVVAIKGLFSGRYLAMNKRGR 104
                                                                                          -PYSQFLSRRNEIPLIHFNTPIPR-----RHTRSAEDDSERDPLNVLKPRARMTPAPA
                                                                                                                      LYASDHYNAE-CEFVERIHELGYNTYASRLYRTGSSGPGAQRQ--PGAQRPWYVSVNGKG 161
                            SCSQELPSAEDNSPMASDPLGVVRGGRVNTHAGG 238
                                                           RPRRGFKTRRTQKSSLF----LPRVLGHKDHEMVRLLQSSQPRAPGEGSQPRQR---
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ROKKOSPGDHGKM--ETLSTRATPSTQLHTGG 241
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                                                                                                                                                                                                                                                                  Similarity
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4225 Executive Square, Suite 1400
                                                                                                                                                                                                                                                                                                                                                                                         245 amino acids
                                                                                                                                                                                                                                                    Conservative
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          : Floppy disk
IBM PC compatible
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                May 12, 1995
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                                                                                                                                                                                                                                                                                                                                                           not relevant
                                                                                                                                                                                                                                                                 13.4%;
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                                                                                                                                                                                                                                                  26;
                                                                                                                                                                                                                                                 Score 182.5; DB 2;
Pred. No. 6.7e-12;
26; Mismatches 88;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      07265/046001
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; Patent No. 645130:
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US-09-417-721-7
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SOFTWARE: PatentIn Ver.
SEQ ID NO 7
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Patent No. 6451303
GENERAL INFORMATION:
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          FILING DATE: 05-JUN-1995
CLASSIFICATION: 536
ATTORNEY AGENT INFORMATION:
NAME: MULLINS, J. G.
REGISTRATION NUMBER: 30,073
REFERENCE/DOCKET NUMBER: 3256
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           APPLICANT: Whitehouse, Martha J.
APPLICANT: Kavanaugh, Michael W.
TITLE OF INVENTION: Angiogenically Effective Unit Dose of FGF and Method of
TITLE OF INVENTION: Administering
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             FILE REFERENCE: 1296/12169US05
CURRENT APPLICATION NUMBER: US/09/417,721
CURRENT FILING DATE: 1999-10-13
PRIOR APPLICATION NUMBER: 60/104,103
PRIOR FILING DATE: 1998-10-13
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      GENERAL INFORMATION:
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                                                                                                                 COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Ve
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/464,590A
FILLING DATE: 05-JUN-1995
                                                                                                                                                                                                                                                  COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
                                                                                                                                                                                                                                                                                                                                                                                                                                                            TITLE OF INVENTION: FIBROBLAST GROWTH FACTOR-11
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        APPLICANT: HU, JING-SHAN
APPLICANT: ROSEN, CRAIG A.
                                                                                                                                                                                                                                                                                                                                                                                                                                           CORRESPONDENCE ADDRESS:
ELECOMMUNICATION INFORMATION
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   222 GKMETLSTRA--TPS 234
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    162 RPRRGFKTRRTOKSSLFLPRVLGHKDHEMVRLLQSSQPRAPGEGSQPRQRRQKKQSPGDH 22:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            102 IFGSHYFDPENCRFQHQTLENGYDVYHSPQYHFLVSLGRAKRAFLPGMNPP------
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                                                                                                                                                                                                                                                                                             COUNTRY: U
                                                                                                                                                                                                                                                                                                                                                                                STREET:
                                                                                                                                                                                                                                                                                                                                                                                               ADDRESSEE: CARELLA, BYRNE, BAIN, GILFILLAN, CECCHI
ADDRESSEE: STEWART & OLSTEIN
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Local Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 56;
                                                                                                                                                                                                                                                                                                                                                          ROSELAND
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Application US/09417721
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                                                                                                                                                                                                                                                                                                                                                                                6 BECKER FARM ROAD
                                                                                                                                                                                                                                                                                                               s.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               28;
                 325800-438
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           IPLIHFNTP-----IPRRHTRSAEDDSER 187
                                                                                                                                                                                    Version
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    DB 4; Length 240;
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US-08-462-169B-11
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                 Query Match
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Query Match 13.3%;
Best Local Similarity 31.0%;
Matches 52; Conservative 2
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             TELEFAX: (201) 994-1744 INFORMATION FOR SEQ ID NO:
                                                                                                                                                                      INFORMATION FOR SEQ ID NO:
                                                                                                                                                                                                                                                                                                                                                                                                                    COMPUTER READABLE FORM:
MEDIUM TYPE: 3.5 INC
COMPUTER: IBM PS/2
                                                                                                                                                    SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                            ATTORNEY/AGENT INFORMATION: NAME: MULLINS, J.G.
                                                                                                                                                                                                                                                                                                                                                CURRENT APPLICATION DATA: APPLICATION NUMBER: US
                                                                   MOLECULE TYPE:
                                                                                                                                                                                                          TELECOMMUNICATION INFORMATION: TELEPHONE: 201-994-1700
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    TOPOLOGY: linear MOLECULE TYPE: protein
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              CORRESPONDENCE ADDRESS:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      154 YSQFLSRRNEIPLIHFNTPIPRRH---TRSAEDDSERDPLNVLKPRAR 198
                                                                                                                                                                                                                                                                                                                                                                                              COMPUTER: IBM PS,
OPERATING SYSTEM:
                                                                                                  STRANDEDNESS
                                                                                                                                                                                                                                          REFERENCE/DOCKET NUMBER: 32,073
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                                                                                     TOPOLOGY:
                                                                                                                       TYPE:
                                                                                                                                                                                           TELEFAX:
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CLASSIFICATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           STREET:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              42 LYTATARNSYHLQIHKNGHVDGAPHQTIYSALMIRSEDAGFVVITGVMSRRYLCMDFRGN 101
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                                                                                                                                    ENGTH:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         TYPE: amino acid
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                                                                                                                       AMINO ACID
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NEW JERSEY
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E: CECCHI, STEWART & OLSTEIN
6 BECKER FARM ROAD
                                                                                                                                      239 AMINO ACIDS
                                                                                                                                                                                           201-994-1744
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/ENTION: Fibroblast Growth Factor-15
                                                                                                                                                                                                                                                                                                                                                                                  SYSTEM: MS-DOS
WORD PERFECT 5.1
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                                                                   PROTEIN
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13.3%;
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Score 180.5;
Pred. No. 1.
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Pred. No. 1.1e-11;
            DB 1;
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            Length 239;
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Matches

52;

Conservative

Mismatches

Indels

15;

Gaps

.1e-11;

Best Local

Similarity

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RESULT 8
US-08-951-822-35
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Best Local Similarity 31.0
Matches 52; Conservative
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APPLICANT: Hu, Ji
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 TELEFAX: 201-994-1744
INFORMATION FOR SEQ ID NO:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          KEGISTRATION NUMBER: 36,134
REFERENCE/DOCKET NUMBER: 325800-100
TELECOMMUNICATION INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  CURRENT APPLICATION DATA:
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MEDIUM TYPE: Floppy disk
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                                                                           164 RRGFKTRRTQKSSLFLPRVLDHRDHEMVRQLQSGLPRPPGKGVQPRRR 211
                                                                                                                                                                                          102 IFGSHYFDPENCRFQHQTLENGYDVYHSPQYHFLVSL-----GRAKRAFLPGMNPP--P 153
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               164 RRGFKTRRTOKSSLFLPRVLDHRDHEMVROLOSGLPRPPGKGVQPRRR 211
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                102 IFGSHYFDPENCRFQHQTLENGYDVYHSPQYHFLVSL-----GRAKRAFLPGMNPP--P
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             APPLICATION NUMBER: US/08/207,412B FILING DATE: 08-MAR-1994 CLASSIFICATION: 435
                                                                                                                                                                                                                                       48
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        OPERATING SYSTEM: PC-DOS/MS-DOS SOFTWARE: Patentin Release #1.0,
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                                                                                                                                                                                                                                                                                                                                                                                                                                                      STRANDEDNESS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          TELEPHONE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    NAME: Ferraro, Gregory D
REGISTRATION NUMBER: 36,
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              COUNTRY:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 CITY: Roseland
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     STREET:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       ADDRESSEE: Carella, Byrne, ADDRESSEE: Stewart & Olste
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             48
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            LENGTH:
                                                                                                                                                      LYASEHYSAE-CEFVERIHELGYNTYASRLYRTVSSTPGARRQPSAERLWYVSVNGKGRP
                                                                                                                 YSQFLSRRNEIPLIHFNTPIPRRH---TRSAEDDSERDPLNVLKPRAR 198
                                                                                                                                                                                                                                   LYCAT---KYHLOLHPSGRVNGSLENSAYSILEITAVEVGIVAIRGLFSGRYLAMNKRGR 104
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INVENTION: Fibr
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                                                                                                                                                                                                                                                                                                              Score 180.5; DB 2;
Pred. No. 1.1e-11;
26; Mismatches 75;
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                                                                                                                                                                                                                                                                                                                                                    Length 239;
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Best Local Similarity
Matches 52; Conserv
                                                                                                                                                                                                                                                                                                                                                       SOFTWARE: PatentIn Ver. 2.0
SEQ ID NO 11
                                                                                                                                                                                                     Matches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Sequence 11, Application US/09103079A Patent No. 6013477
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Sequence 35, Application US/08951822A
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                APPLICANT: Greene, John M.
APPLICANT: Rosen, Craig A.
TITLE OF INVENTION: Fibroblast Growth Factor
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       APPLICANT: Raymond, Fewer-APPLICANT: Bukowski, Thomas R. APPLICANT: Holderman, Susan D.
                                                                                                                                                                                                                                                                                                                                                                                                                                     CURRENT FILING DATE: 1998-06-23
EARLIER APPLICATION NUMBER: 08/462,169
                                                                                                                                                                                                                                                                                                                                                                                            NUMBER OF SEQ ID NOS: 32
                                                                                                                                                                                                                                                                                                                                                                                                                     EARLIER FILING DATE: 1995-06-05
                                                                                                                                                                                                                                                                                                                                                                                                                                                                            CURRENT APPLICATION NUMBER: US/09/103,079A
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  FILE REFERENCE: PF203D1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         FILE REFERENCE: 96-20
CURRENT APPLICATION NUMBER: US/08/951,822A
CURRENT FILING DATE: 1997-10-16
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APPLICANT: Sheppard, Paul O.
TITLE OF INVENTION: NOVEL FGF HOMOLOGS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           NUMBER OF SEQ ID NOS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        APPLICANT: Conklin, Darrell
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        APPLICANT: Deisher, Theresa
                                                                                                                                                                                                                                                                                              TYPE: PRT
ORGANISM: Homo sapiens
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              LENGTH: 239
TYPE: PRT
                                                                                                                                                                                                                                                                                                                                         LENGTH: 239
154 YSQFLSRRNEIPLIHFNTPIPRRH---TRSAEDDSERDPLNVLKPRAR 198
                                    105 LYASEHYSAE-CEFVERIHELGYNTYASRLYRTVSSTPGARROPSAERLWYVSVNGKGRP 163
                                                                             102 IFGSHYFDPENCRFQHQTLENGYDVYHSPQYHFLVSL-----GRAKRAFLPGMNPP--P 153
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                                                                                                                                                                                                                   Local
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                                                                                                                                              42 LYTATARNSYHLQIHKNGHVDGAPHQTIYSALMIRSEDAGFVVITGVMSRRYLCMDFRGN 101
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                                                                                                                 LYCAT---KYHLOLHPSGRVNGSLENSAYSILEITAVEVGIVAIRGLFSGRYLAMNKRGR 104
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                                                                                                                                                                                                                     Similarity
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31.0%; Pred. No. 1.1e-11;
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                                                                                                                                                                                                                 Score 180.5; DB 3
Pred. No. 1.1e-11;
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                                                                                                                                                                                                                                   Length 239;
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Best Local S
                                                                                               Sequence 21,
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                                                          GENERAL INFORMATION:
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INFORMATION FOR SEQ ID NO:
SEQUENCE CHARACTERISTICS:
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OTHER INFORMATION: /note= "FGF-3"
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PILING DATE: 24-SEP-1996
CLASSIFICATION: 424
ATTORNEY/AGENT INFORMATION:
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OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0,
CURRENT APPLICATION DATA:
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COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
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APPLICANT: Sosnowski, Barbara A.
TITLE OF INVENTION: COMPOSITIONS CONTAINING NUCLEIC ACIDS AND LIGANDS FOR THERAPE
NUMBER OF SEQUENCES: 128
CORRESPONDENCE ADDRESS:
                                        APPLICANT:
                         APPLICANT:
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     PPLICANT:
                                                                                                                                                                                      164 RRGFKTRRTOKSSLFLPRVLDHRDHEMVRQLQSGLPRPPGKGVQPRRR 211
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                                                                                                                                                                                                                                                                                                                                                                                                                                        Local Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               NAME: No. 6037329tenburg Ph.D., Carol REGISTRATION NUMBER: 39,317 REFERENCE/DOCKET NUMBER: 760100.415C1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          TOPOLOGY:
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                                                                                                                                                                                                                                                                LYASEHYSAE-CEFVERIHELGYNTYASRLYRTVSSTPGARRQPSAERLWYVSVNGKGRP
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                                                                                               Application US/09023082A
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             239 amino acids
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(206) 682-6031
Th NO: 12:
   JIMENEZ, PABLO
DUAN, D. ROXANNE
                                        RUBEN, STEVEN M.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          unknown
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Pred. No. 1.1e-11;
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US-09-023-082A-21
                                                  Query Match
Best Local Similarity
                                     Matches
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                                                                                                                 TOPOLOGY: no
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APPLICANT:
APPLICANT:
                                                                                                                                                                                                    SEQUENCE CHARACTERISTICS:
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PRIOR APPLICATION NUMBER: US 08/461,195
                                                                                                                                                                                                                                                                                                                                   ATTORNEY/AGENT INFORMATION:
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CURRENT APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
                                                                                                                                                                                                                                                  TELECOMMUNICATION INFORMATION: TELEPHONE: 202-371-2600
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APPLICATION NUMBER: US 60/023,852
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42 LYTATARNSYHLOIHKNGHVDGAPHOTIYSALMIRSEDAGFVVITGVMSRRYLCMDFRGN 101
                                                                                                                                                STRANDEDNESS:
                                                                                                                                                                                                                                                                                                                                                                                                  APPLICATION NUMBER: US 0 FILING DATE: 13-AUG-1997
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CITY: WASHINGTON
                                                                                                                                                                                                                                                                                    REFERENCE/DOCKET NUMBER:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    APPLICATION NUMBER: US/09/023,082A
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NT: GRUBER, JOACHIM R.
NT: DILLON, PATRICK J.
NT: GENTZ, REINER L.
F INVENTION: KERATINOCYT
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                                     Conservative
                                                                                                                                                                                                                                    202-371-2540
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MOORE, PAUL A.
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SYSTEM: PC-DOS/MS-DOS
                                                                                                                                                                                   amino acids
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                                               13.3%; Score 180.5; DB 31.0%; Pred. No. 1.1e-11
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                                                                                                                                                                                                                                                                                                                                                                  US 60/055,561
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                                                                                                                                                                                                                                                                                                   36,688
                                26; Mismatches
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                                                              DB 3;
                                Indels
                                                                Length
                                                                  239;
                                15;
                                Gaps
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102 IFGSHYFDPENCRFQHQTLENGYDVYHSPQYHFLVSL-----GRAKRAFLPGMNPP--P 153

48 LYCAT---KYHLQLHPSGRVNGSLENSAYSILEITAVEVGIVAIRGLFSGRYLAMNKRGR 104

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Query Match
Best Local Similarity
Watches 52; Conserve
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US-09-368-951-35
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US-09-093-585-11
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08
FILING DATE: 05-JUN-1995
ATTORNEY/AGENT INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           COMPUTER READABLE FORM: MEDIUM TYPE: Floppy disk
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         TELECOMMUNICATION INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         CURRENT APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        TITLE OF INVENTION: FIBROBLAST GROWTH FACTOR-11
NUMBER OF SEQUENCES: 17
CORRESPONDENCE ADDRESS:
                                                                                      164 RRGFKTRRTQKSSLFLPRVLDHRDHEMVRQLQSGLPRPPGKGVQPRRR 211
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          164 RRGFKTRRTQKSSLFLPRVLDHRDHEMVRQLQSGLPRPPGKGVQPRRR 211
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                                                                                                                       154 YSQFLSRRNEIPLIHFNTPIPRRH---TRSAEDDSERDPLNVLKPRAR 198
                                                                                                                                                        105 LYASEHYSAE-CEFVERIHELGYNTYASRLYRTVSSTPGARRQPSAERLWYVSVNGKGRP 163
                                                                                                                                                                                             102 IFGSHYFDPENCRFQHQTLENGYDVYHSPQYHFLVSL-----GRAKRAFLPGMNPP--P 153
                                                                                                                                                                                                                                48 LYCAT---KYHLQLHPSGRVNGSLENSAYSILBITAVEVGIVAIRGLFSGRYLAMNKRGR 104
                                                                                                                                                                                                                                                                 42 LYTATARNSYHLQIHKNGHVDGAPHQTIYSALMIRSEDAGFVVITGVMSRRYLCMDFRGN 101
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                                                                                                                                                                                                                                                                                                                                                                                                                            STRANDEDNESS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          NAME: MULLINS, J. G.
REGISTRATION NUMBER: 30,073
REFERENCE/DOCKET NUMBER: 32
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       CLASSIFICATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       APPLICATION NUMBER: US/09/093,585
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
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35, Application US/09368951
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ROSEN, CRAIG A.
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                                                                                                                                                                                                                                                                                                                                                                                                               linear
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994-1744
NO: 11:
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                                                                                                                                                                                                                                                                                                                       13.3%; Score 180.5; 31.0%; Pred. No. 1.:
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US-08-438-439C-17
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Best Local Similarity
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         CURRENT APPLICATION NUMBER: US/09/368,951
CURRENT FILING DATE: 1999-08-05
EARLIER APPLICATION NUMBER: 08/951,822
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  APPLICANT: Sheppard, Paul O.
TITLE OF INVENTION: NOVEL FGF HOMOLOGS
FILE REFERENCE: 96-20
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TYPE: PRT
                                                                                                                                             SOFTWARE: PatentIn Rel
                                                                                                                                                                                                                      COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
                                                                      ATTORNEY/AGENT INFORMATION:
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                                                                                                                                                                                                                                                                                      ADD<sub>K</sub>
STREET:
TITY: La Jo.
CA
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NAME: Haile, Lisa A.
REGISTRATION NUMBER: 38,347
REFERENCE/DOCKET NUMBER: 077
ELECOMMUNICATION INFORMATION:
                                                                                          APPLICATION NUMBER: FILING DATE: May 1: CLASSIFICATION: 43
                                                                                                                                                                                    COMPUTER: IBM PC compatible OPERATING SYSTEM: PC-DOS/MS-DOS
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              42 LYTATARNSYHLQIHKNGHVDGAPHQTIYSALMIRSEDAGFVVITGVMSRRYLCMDFRGN 101
                                                                                                                                                                                                                                                                                COUNTRY:
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                                                                                                                                                                                                                                                                                                                                    E: Fish & Richardson P.C.
4225 Executive Square, Suite 1400
                                                                                                                                                                                                                                                                                                                 Jolia
                                                                                                                                                                                                                                                                              USA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Smallwood, Phillip M.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Nathans, Jeremy
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                                                                                          May 12, 1995
N: 435
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                                                                                                                                                                                                                                                                                                                                                                                                                FIBROBROBLAST GROWTH FACTOR HOMOLOGOUS FACTOR-2 AND METHODS OF USE
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31.0%; Fred. No. 1.1e-11;
                                                                                                                                US/08/438,439C
                                                                                                                                                                   Release #1.0,
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Best Local Similarity
Matches 70; Conserv
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INFORMATION FOR SEQ ID NO: 1
SEQUENCE CHARACTERISTICS:
LENGTH: 245 amino acids
TELEFAX: (617) 861-9540
NFORMATION FOR SEQ ID NO: 15:
                                       TELEPHONE: (617) 861-6240
                                                                                                                                   CLASSIFICATION: 435
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/279,217
FILING DATE: 22-UUL-1994
ATTORNEY AGENT INFORMATION:
                                                                                                                                                                                                                                     COMPUTER READABLE FORM:
MEDLIM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOSTWARE: PATENTIA Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/441,629
FILLING DATE: 15-MAY-1995
CIASCIETCATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    APPLICANT: Kirschner, Marc W.
APPLICANT: Kinoshita, No. 5766923iyuki
TITLE OF INVENTION: RECEPTOR-LIGAND ASSAY
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      TOPOLOGY: linear MOLECULE TYPE: protein
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        NUMBER OF SEQUENCES: 1
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            126 VYHSPQYHFIVSLGRAKRAFIPGMNPP------PYSQFLSRRNBIPLIHFNTPIPR 175
                                                                           NAME: Granahan, Patricia
REGISTRATION NUMBER: 32,227
REFERENCE/DOCKET NUMBER: HU95-01A
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         19 MSVLR-AYPNASP-----LLGSSWGGLIHLYTATAR-----NSYHLQIHKNGHVDGAP 65
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      69 ENSAYSILEITAVEVGGVAIKGLFSGRYLAMNKRGRLYASDHYNAE-CEFVERIHELGYN 127
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         66 HQTIYSALMIRSEDAGFYVITGVMSRRYLCMDFRGNIFGSHYFDFENCRFQHQTLENGYD 125
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STRANDEDNESS: not
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            DDRESSEE:
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                                                                                                                                                                                                                                                                                                                                                                                                                                               Massachusetts
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                                                                                                                                                                                                                                                                                                                                                                                                                               USA
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28.0%; Pred. No. 1.1
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                                                                                                                                                                                                                                  Query Match 12.9%;
Best Local Similarity 35.6%;
Matches 47; Conservative 1
                                                                                                                                                                                                                                                                          Query Match
                                                                                                                                                                                                                                                                                                                                 TYPE: amino acid
STRANDEDNESS: single
TOPOLOGY: linear
MOLECULE TYPE: protein
162 RPRRGFKTRRTO 173
                                      153 - PYSQFLSRRNE 163
                                                                          105 LYASDHYNAE-CEFVERIHELGYNTYASRLYRTGSSGPGAQRQ--PGAQRPWYVSVNGKG 161
                                                                                                                102 IFGSHYFDPENCRFQHQTLENGYDVYHSPQYHFLVSLGRAKRAFLPGMNPP----- 152
                                                                                                                                                      48 LYCAT---KYHLOLHPSGRVNGSLENSAYSILEITAVEVGVVAIKGLFSGRYLAMNKRGR 104
                                                                                                                                                                                          42 LYTATARNSYHLQIHKNGHVDGAPHQTIYSALMIRSEDAGFVVITGVMSRRYLCMDFRGN 101
                                                                                                                                                                                                                                  19; Mismatches
                                                                                                                                                                                                                                                    Score 176; DB 1;
Pred. No. 2.2e-11;
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Search completed: May 23, 2003, 07:46:21 Job time : 31 secs

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Run
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Maximum Match 100%
Listing first 45 summaries
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Maximum DB seq length: 200000000
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Perfect score:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Searched:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Scoring table:
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1360
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L: /SIDS2/gcgdata/
/SIDS2/gcgdata/geneseq/geneseqp-emb1/AA199.DAT:
/SIDS2/gcgdata/geneseq/geneseqp-emb1/AA2000.DAT:
/SIDS2/gcgdata/geneseq/geneseqp-emb1/AA2000.DAT:
/SIDS2/gcgdata/geneseq/geneseqp-emb1/AA2000.DAT:
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Pred. No. is the number of results predicted by score greater than or equal to the score of the and is derived by analysis of the total score di chance to have a result being printed,

SUMMARIES

14-FEB-2000; 2000US-0182172 29-FEB-2000; 2000US-0186084 '18-APR-2000; 2000US-0198583

45	44	43	42	41	40	39	38	37	36	35	ω 4	ω G	32	31	30	29	28	27	26	25	24	23	22	21	20	19	18	17	16	15	14	13	12	11
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209	209	208	208	208	208	210	210	210	210	72	180	149	155	177	251	251	251	178	178	248	229	227	227	233	251	251	251	251	251	251	251	251	251	251
22	22	23	23	22	23	23	22	22	21												23	23	22	22	23	23	23	23	23	23	23	23	23	23
AAB82351	AAB83951	760	63	AAE05078	AAU79290	AAE24375	AAU00958	AAB68416	AAB18636	ABB06943	ABB06944	ABB81314	ABB06942	AAY85637	AAU79356	AAG63946	AAG63945	AAY85639	63	ABB06951	ABB06952	94	581	AAB85829	758	œ	ABB77585	58	38	7	œ	5	ABB08352	ABB06940
JAFFA	aci	extracell	PRO protein	an fibroblast	GF-related	n FGF-21 prot	H	Ø	acid sequen	OST311 prot	OST311 prot	FGF23 core	DST311 pro	ey fibroblast	fibro	acid	acid sequen	Human fibroblast g	Human fibroblast q	orot	T311 protein	lprot	fibroblas	fib		fib	FGF23 muta	FGF23 mutan	fibroblast	fibroblas	FGF23	FGF23 mutant	zFGF12 amin	Human OST311 prote

ALIGNMENTS

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Human sbgFGF-19b protein.
                                       19-NOV-2001
                                                                                                             AAE09459 standard; Protein; 251 AA.
                                   (first entry)
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RESULT 1
AREOGRAM
ARE Human; Alzheimer's disease; amyotrophic lateral sclerosis; ALS; Zollinger-Ellison syndrome; immune system disease; schizophrenia; inflammation; haematopoietic disease; anxiety; feeding disorder; aging; anorexia, depression; cardiovascular disease; sleep disorder; seizure; memory alteration; migraine; stroke; asthma; neuropathy; hypoglycaemia; sexual disorder; growth abnormality; infection; autoimmune disease; rheumatoid arthritis; cataractogenesis; angiogenesis; atherosclerosis; cerebral ischaemia; cirrhosis; Huntington's disease; Hodgson's disease, hypercholesterolaemia; headache; amnesia; cardiac arrhythmia; obesity; diabetes mellitus; glomerulonephritis; renovascular hypertension; cancer; vaccine; gene therapy; sbgFGF-19b gene 14-FEB-2001; 2001WO-US04703 23-AUG-2001. Homo sapiens. WO200160850-A1.

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                                                                                                                                                                                                                                                                                                                                                                                                                                       cc amyotrophic lateral sclerosis (ALS), Zollinger-Elison syndrome, diseases cof the immune system, haematopoietic disease, inflammation, anxiety, eschizophrenia, feeding disorders, anorexia, depression, social, sexual cc and rewarded behaviour, cardiovascular disease, sleep disorder, learning and memory alteration and altered immune response, seizure, migraine, cc cancer, stroke, asthma, neuropathy, aging, sexual disorders, treatment of transsexuals, growth abnormalities, obesity, infections, autoimmune cd diseases (e.g. rheumatoid arthritis), cataractogenesis, angiogenesis, disorders associated with healthy maintenance of gastric mucosa and creative action activates and chronic mucosal lesion, lung carcinoma, cerebral ischaemia, atherosclerosis, cirrhosis, Huntington's disease, headache, camnesia, multiple sclerosis, lodgson's disease, dilated cardiomyopathy, congestive heart failure, cardiac arrhythmias, hypercholesterolaemia, viral and non-viral hepatitis, type I and type II diabetes mellitus, cl paralyses, tendinitis and malignant hyperthermia. Polypeptides of the invention are used to identify membrane bound and soluble receptors. They are also useful as vaccines for inducing an immunological response in a mammal. Polynucleotides of the invention are used in gene therapy.
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Best Local :
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                The invention relates to secreted and membrane associated polypeptides and nucleic acid molecules encoding such polypeptides. Sequences of the invention are useful for treating diseases such as Alzheimer's disease,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  New secreted and membrane associated polypeptides for treating Alzheimer's disease, psoriasis, cancer, enterocolitis, sleep and sexual disorders, stroke, and asthma
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     They are also valuable for chromosome localisation studies
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             The present sequence is a human sbgFGF-19b protein,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Agarwal P,
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                                                                                                                                                                                                                                 VDGAPHQTIYSALMIRSEDAGFVVITGVMSRRYLCMDFRGNIFGSHYFDPENCRFQHQTL
                                                                                                                                                                                                                                                                                                            MLGARLRLMVCALCSVCSMSVLRAYPNASPLLGSSWGGLIHLYTATARNSYHLQIHKNGH
                                                                                             AEDDSERDPLNVLKPRARMTPAPASCSQELPSAEDNSPMASDPLGVVRGGRVNTHAGGTG
                                                                                                                                                          ENGYDYYHSPQYHFLVSLGRAKRAFLPGMNPPPYSQFLSRRNEIPLIHFNTPIPRRHTRS
                                                                                                                                                                                                                                                                                   MLGARLRLWVCALCSVCSMSVLRAYPNASPLLGSSWGGLIHLYTATARNSYHLQIHKNGH
                                   PEGCRPFAKFI
                                                                                                                                        ENGYDVYHSPQYHFLVSLGRAKRAFLPGMNPPPYSQFLSRRNEIPLIHFNTPIPRRHTRS
                                                                                                                                                                                                             VDGAPHQTIYSALMIRSEDAGFVVITGVMSRRYLCMDFRGNIFGSHYFDPENCRFQHQTL
                                                                   AEDDSERDPLNVLKPRARMTPAPASCSQELPSAEDNSPMASDPLGVVRGGRVNTHAGGTG
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                        studies.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            protein of the invention.
                                                                                                                                                                                                                                                                                                                                                                                                                                     251 AA;
                                                                                                                                                                                                                                                                                                                                                              Conservative
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251
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BEECHAM PLC.
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Pred. No. 7.5e-131;
                                                                                                                                                                                                                                                                                                                                                            Mismatches
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RESULT 2 AAB85810 ID AAB8

AAB85810 standard; Protein; 251

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Best Local
                                                                                                                                                                                                                                                                                                              This represents a human fibroblast growth factor (FGF)-23 polypeptide. The DNA insert is contained in ATCC Deposit No. PTA-1617. FGF-23 can be expressed by standard recombinant methodology. The FGF-23 polypeptides, polynucleotides, modulators and antibodies are useful for treating, preventing, or ameliorating an FGF-23 polypeptide-related disease, condition or disorder especially autosomal dominant hypophosphatemic rickets (ADHR). They are also useful for diagnosing a pathological condition and for stimulating angiogenesis, promotting wound healing and treating disorders of the liver.
                                                                                                                                                                                                                                                                                        Sequence
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    15-FEB-2000; 2000US-0182442
20-APR-2000; 2000US-0198903
15-FEB-2001; 2001US-0748581
                                                                                                                                                                                                                                                                                                                                                                                                                                                             Claim 15; Fig 1A-B;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         An isolated nucleic acid molecule encoding a fibroblast growth fact 23 useful for treating autosomal dominant hypophosphatemic rickets
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   WPI; 2001-514774/56.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Luethy R,
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            23-AUG-2001.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Fibroblast growth factor; FGF; FGF-23; osteopathic; vulnerary; ADHR; hepatotropic; autosomal dominant hypophosphatemic rickets; human; angiogenesis; gene-therapy; liver disorder; antisense-therapy.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Human fibroblast growth factor (FGF)-23
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        29-OCT-2001
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                                                         121
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           (AMGE-) AMGEN INC
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                                                                                                                                                                                                MLGARLRLWVCALCSVCSMSVLRAYPNASPLLGSSWGGLIHLYTATARNSYHLQIHKNGH 60
                AEDDSERDPLNVLKPRARMTPAPASCSQELPSAEDNSPMASDPLGVVRGGRVNTHAGGTG
                                                                                                                                                                    MIGARLRIMVCALCSVCSMSVLRAYPNASPLIGSSWGGLIHLYTATARNSYHLQIHKNGH
                                                                        ENGYDVYHSPQYHFLVSLGRÆKRAFLFGMNPPPYSQFLSRRNEIPLIHFNTPIPRRHTRS
                                                                                                                               VDGAPHQTIYSALMIRSEDAGFVVITGVMSRRYLCMDFRGNIFGSHYFDPENCRFQHQTL 120
 AEDDSERDPLNVLKPRARMTPAPASCSQELPSAEDNSPMASDPLGVVRGGRVNTHAGGTG
                                                      ENGYDVYHSPQYHFLVSLGRAKRAFLPGMNPPPYSQFLSRRNEIPLIHFNTPIPRRHTRS
                                                                                                             VDGAPHQTIYSALMIRSEDAGFVVITGVMSRRYLCMDFRGNIFGSHYFDPENCRFQHQTL
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                note= "specifically claimed mature protein"
                                                                                                                                                                                                                                                                                                                                                                                                                                                             158pp; English.
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Pred. No. 7.5e-131;
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251

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RESULT 3
AAG63944
                                           The present sequence represents fibroblast growth factor 23 (FGF-23). CC Human FGF-23 polymucleotides and polypeptides are useful for treating captient suffering from traumatic injury or a condition characterized by dysfunction of or injury to skin cells, a condition characterized by CC inadequate function of placental cells (e.g. congenital defects, CC fertility, or abnormal growth), a condition characterized by inadequate function of the thymus, a condition characterized by concision of the thymus, a condition characterized by inadequate function of the thymus, a condition characterized by inadequate contiferative disorder of the thymus, or differentiation disorder of the thymus, or differentiation disorder of the thymus, or a condition characterized by central nervous system conditions, a condition characterized by central nervous system conditions, and constant of sease, and intestinal wounds, ulcers, inflammation, CC disorder (e.g. Parkinson's disease or Alzheimer's disease, in the treatment conformation and surgical anastomoses, motility and absorption disorders, and congenital malformations of the intestine. They are also useful for treating ischemic vascular diseases, enal artery disease, stroke) and congenital disease, renal artery disease, stroke) and constitution or death of skeletal muscle cells, hone cells or supporting constitution or death of skeletal muscle cells, hone cells or supporting constitution or death of skeletal muscle cells, bone cells or supporting constitutions.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                          Claim 12; Fig 3; 77pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Isolated nucleic acids encoding the human and murine fibroblast (factor 23, useful in the treatment of a condition characterized linadequate function of placental cells (e.g. congenital defects) the thymus (e.g. leukemia)
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18-SEP-2000; 2000US-0233368.
05-DEC-2000; 2000US-0251649.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Fibroblast growth factor 23; FGF-23; injury; placental cell; ulcer; congenital defect; fertility; abnormal growth; thymus function; leukemla; lymphoma; autoimmune disease; proliferative disorder; infarction; differentiation disorder; central nervous system disorder; infarction; parkinson's disease; Alzheimer's disease; Crohn's disease; inflammation; intestinal wound; motility disorder; absorption disorder; stroke; congenital malformation; ischemic vascular disease; myocardial ischemia; peripheral vascular disease; renal artery disease; bone disease;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                07-MAR-2001; 2001WO-US07469
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              musculoskeletal disease; skeletal myopathy; arthritis.
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                                    skeletal myopathies,
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                                    bone disease, or
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Sequence

Claim 12; Fig 3; 77pp; English

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RESULT 4
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18-SEP-2000; 2000US-0233368.
05-DEC-2000; 2000US-0251650.
                                                                   factor 23, useful in the treatment of a condition characterized inadequate function of placental cells (e.g. congenital defects) the thymus (e.g. leukemia) -
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                                                                                                                                                        solated nucleic acids encoding the human and murine fibroblast
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Pred. No. 7.5e-131;
; Mismatches 0;
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RESULT 5
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Best Local
 01-DEC-1999;
01-DEC-1999;
                                                   01-DEC-2000; 2000WO-US32678
                                                                                                                                                                                                                  breast; prostate; cervical; tumour necrosis factor-alpha; TNF-alpha; cartilage; ear; proliferation; glucose; free fatty acid; skeletal muscle;
                                                                                                                                                                                                                                                                                                                                24-OCT-2001 (first entry)
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                                                                                                                                                                Homo sapiens
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                                                                                                                                                                                                                                                                                            Human PR09828 polypeptide sequence
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             of function, inadequate runction of tweether, bone disease, cells or supporting cells (e.g. skeletal myopathies, bone disease,
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                                                                                                                                                                                                                                                        secretory and transmembrane; PRO; mammalian;
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99WO-US28634
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Pred. No. 7.5e-131;
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30-MAR-2000;
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24-FEB-2000;
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99WO-US30999
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Gerritsen Smith V, Ğ, M Stewart TA, Beresini M, ME, Goddard I A, Godowa Tumas D, Deforge L, Desnoyers L, Filvaroff E, A, Godowski PJ, Gurney AL, Sherwood S; Numas D, Watanabe CK, Wood WI, Zhang Z Gao

WPI; 2001-408281/43. N-PSDB; AAS21376.

Isolated, secretory and transmembrane PRO polypeptide used to detect other PRO polypeptides, link bioactive molecules to cells expressing PRO polypeptides, and detect the presence of mammalian tumours e.g. lung, breast, prostate, cervical

Claim 12; Fig 266; 813pp; English

CC PRO polypeptides, and to detect the presence of mammalian lung, colon, CC breast, prostate, rectal, cervical or liver tumours by comparing PRO CC polypeptide expression in a cell sample to that in a control sample. CC Some of the 275 sequences are also useful to stimulate the release of the under necrosis factor-alpha (TNF-alpha) from human blood, the control sample. CC proliferation or differentiation of chondrocytes, the proliferation or control sequences are associated to stimulate the release of control sequences from cc cartilage, the proliferation of inner ear utricular supporting cells or control sequences, the release of proteoglycans from cc cartilage, the proliferation of inner ear utricular supporting cells or conforted to the proliferation of a cytokine from peripheral blood connocytes (PBMCs), or the proliferation of endothelial cells. Some of the PRO polypeptides may modulate glucose or free fatty acid uptake by conscitute the proliferations. The factor VIIA. The PRO polypeptides can be used in assays to identify consciules involved in binding interactions. The polymcleotides encoding PRO polypeptides can be used in assays to identify consciules involved in binding interactions. The polymcleotides encoding PRO polypeptides can be used in gene therapy. AAU12172-AAU12446 represent novel human secretory and transmembrane PRO polypeptides. The PRO polypeptides are useful to detect other PRO polypeptides, to link bioactive molecules to cells expressing PRO polypeptides, to modulate biological activities of cells expressing

Sequence 251 A A

Ś Matches Query Match Best Local MLGARLRLWVCALCSVCSMSVLRAYPNASPLLGSSWGGLIHLYTATARNSYHLQIHKNGH 60 Similarity Conservative 100.0%; 0 Score 1360; DB 22; Pred. No. 7.5e-131; ; Mismatches 0; Indels Length 0, Gaps

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RESULT 6
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                                     The present sequence represents a human fibroblast growth factor (FGF) homologue, designated zFGF12. The zFGF12 polypeptides contain a motif (see AAB84654) that occurs in all known members of the FGF family, which is unique to these proteins. This motif is highly conserved in all members of the FGF family, however, zFGF12 appears to be unique in that the conserved Glu is a His (residue 117) substituting a basic amino acid (aa) residue for an acidic aa residue. The zFGF12 gene is mapped to chromosome 12, location 12q.1.3. zFGF12 may be used in the
prevention, diagnosis and treatment of diseases associated with inappropriate FGF expression. Disorders and processes that may l prevented, diagnosed, and treated include, for example prolifer.
                                                                                                                                                                                                                 A fibroblast growth factor homolog polypeptide zFGF12 and the nucleic acids that encode it, useful for preventing, diagnosing and controlling e.g. diabetes, amylotrophic lateral sclerosis, strokes, angiogenesis
                                                                                                                                                                                                                                                                                   WPI; 2001-418357/44.
N-PSDB; AAH28133.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 sequence of fibroblast growth factor homologue zFGF12.
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RESULT 7
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Best Local (
Full length GENSET human nucleic acids encoding potentially secreted proteins, useful in gene therapy and vaccination against a variety of diseases, and for diagnosis of those diseases.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            of neuronal, prostatic and pancreatic tissue cells, growth and differentiation of haematopoietic cells, hyperplasia and regeneration, diabetes, amylotrophic lateral sclerosis, strokes, angiogenesis and
                                                                                                                                                                                                                                 08-DEC-1999; 99US-0169629
06-MAR-2000; 2000US-0187470
                                                                  Claim
                                                                                                                                           N-PSDB; AAH64781.
                                                                                                                                                                                 Dumas Milne Edwards
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                                                                                                                                                                                                                                                                                                                            WO200142451-A2
                                                                                                                                                                                                                                                                                                                                                                               GENSET
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potentially secreted proteins. The nucleic they encode may be used in the prevention, diseases associated with inappropriate GEN

nucleic acids encoding

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Best Local S
Matches 251
                        02-JUN-1999;
23-JUN-1999;
07-JUL-1999;
20-JUL-1999;
26-JUL-1999;
26-JUL-1999;
17-AUG-1999;
15-SEP-1999;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Human; secre
cell death;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Human PRO9828 protein sequence SEQ ID NO:511.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      AAB65297 standard; Protein;
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                                                                                                                                                                                                                                                                     30-MAR-2000;
                                                                                                                                                                                                                                                                                                                                                                                WO200073454-A1
                                                                                                                                                                                                                                                                                                                                                                                                                                     Homo
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   diagnostic assay.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            cancer;
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                                                                                                                                                                                                                                                                     2000WO-US08439
99WO-US12252.
99US-0141037.
99US-0143048.
99US-0144758.
99US-0146598.
99US-0146529.
99US-0146529.
99US-014939.
99WO-US21090.
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Pred. No. 7.5e-131;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            mapping; gene
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  PRO; cytostatic;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       mapping; tissue typing;
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18-FEB-2000;
22-FEB-2000;
24-FEB-2000;
24-FEB-2000;
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30-NOV-1999;
01-DEC-1999;
16-DEC-1999;
20-DEC-1999;
                                        sequences, and their fragments, can be used as hybridisation probes, in chromosomal and gene mapping, and in the generation of anti-sense RNA and DNA. They may also be used to produce transgenic animals which are used to develop and screen therapeutically useful reagents. The PRO nucleotide and protein sequence can be used for tissue typing and in treating cancer. Anti-PRO antibodies can be used in diagnostic assays. AAF44270 to AAF4470 PRO sequences and hybridisation probes used in the isolation of human PRO sequences. AAF44087 to AAF44269 and AAB65154 to AAB65300 represent human PRO polynucleotide and protein
                                                                                                                                                                                                                                                                                             PRO polynucleotides used to produce polypeptides used to target bioactive molecules such as toxins, radiolabels or antibodies, specific cells, to cause targeted cell death -
                                                                                                                                                                                   The present invention describes human secreted and transmembrane PRO proteins. The PRO proteins have cytostatic activity. The PRO proteins can be used for targeted delivery of bloactive molecules, such as toxins, radiolabels or antibodies, that cause cell death. PRO nucleotide
                                                                                                                                                                                                                                                                                                                                                                                                                       Ashkenazi AJ, Baker KP, Botstein D, Desnoy, Ferrara N, Fong S, Gezber H, Gerritsen MF, Grimaldi CJ, Gurney AL, Kljavin IJ, Napier Roy MA, Stewart TA, Tumas D, Watanabe CK,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            05-JAN-2000;
06-JAN-2000;
 Sequence
                                                                                                                                                                                                                                                                Claim 12; Fig 324; 935pp; English
                                                                                                                                                                                                                                                                                                                                                             N-PSDB;
                              sequences
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DB; AAF44266.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      GENENTECH INC.
                            given in the
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2000WO-US00376
2000WO-US003565
2000WO-US04341
2000WO-US04414
2000WO-US04914
2000WO-US05004
2000WO-US05841
2000WO-US05884
2000WO-US05884
2000WO-US058884
2000WO-US073777
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99WO-US28313.
99WO-US28301.
99WO-US30095.
99WO-US30911.
AA;
                            exemplification of the present invention.
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be CK, Williams
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                                                                                                                                                                     VDGAPHQTIYSALMIRSEDAGFVVITGVMSRRYLCMDFRGNIFGSHYFDPENCRFQHQTL 120
                                                               AEDDSERDPLNVLKPRARMTPAPASCSQELPSAEDNSPMASDPLGVVRGGRVNTHAGGTG
                                                                                                                                                     VDGAPHQTIYSALMIRSEDAGFVVITGVMSRRYLCMDFRGNIFGSHYFDPENCRFQHQTL
                                                                                                                                                                                                        MLGARLRLWVCALCSVCSMSVLRAYPNASPLLGSSWGGLIHLYTATARNSYHLQIHKNGH
                        PEGCRPFAKFI
                                                                                                  ENGYDVYHSPQYHFLVSLGRAKRAFLPGMNPPPYSQFLSRRNEIPLIHFNTPIPRRHTRS
                                                 AEDDSERDPLNVLKPRARMTPAPASCSQELPSAEDNSPMASDPLGVVRGGRVNTHAGGTG
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251
                        251
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RESULT 9
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AC ABB7
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Best Local :
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               tryptophan. The mutants are generated by introducing the following base changes in the nucleic acid sequence: R176Q mutant is generated by G527A; R179Q is generated by G536A; and R179W is generated by C535T. The protein and encoding DNA are applicable in remedies for
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Sequence
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        The invention relates to a DNA (ABN81575) encoding a protein (ABB77581) FGF23 and mutants FGF23 comprising an amino acid substitution of arginine at position 176 to glutamine and/or position 179 to glutamine or
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Human FGF23 protein mutant applicable in gene therapy
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Claim 1; Page 46-48; 64pp; Japanese.
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29-MAY-2001; 2001JP-0161370.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 251 AA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Conservative
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    for lowering blood phosphorus level, remedies for hyperphosphatemia -
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      ĕ
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Score 1360; DB 23;
Pred. No. 7.5e-131;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               gene therapy.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Mismatches
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                                                                                calcinosis. Osteoporosis, conditions (e.g., dermatomyositis) involving deposition of calcium and phosphate in the arteries or soft tissues of mammal, coronary artery disease may also be treated using methods described in the invention. Preferably, the nucleic acid or the polypeptide comprises a mutation that confers increased stability on FGF23 polypeptide. The polynucleotide encoding (I) can be used in gene therapy to treat diseased individuals. This is the amino acid sequence of the novel human fibroblast growth factor 23 (FGF23) studied in the
                                                                                                                                                                                                                                                                                                                                               The invention describes an isolated polypeptide (I) comprising a fibroblast growth factor 23 (FGF23) polypeptide or its mutant, variant, homologue or fragment. (I) is useful for treatment of a hypophosphataemic disorder such as autosomal dominant hypophosphataemic rickets (ADHR), X-linked hypophosphataemic rickets (XLH), hereditary hypophosphataemic rickets with hypercalciuria (HHRH), hypophosphataemic bone disease (HBD), epidermal nevus syndrome, fibrous dysplasia tumour induced osteomalacia (TIO), and nephrolithiasis. (I) can also be used in treatment of a hyperphosphataemic disorder such as mild renal insufficiency and tumoural
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Novel fibroblast growth factor 23, and polynucleotides encoding the polypeptides, useful for treating hyperphosphataemic disorders such mild renal insufficiency or tumoural calcinosis, or coronary artery
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Pibroblast growth factor 23; PGP23; hypophosphataemic disorder; autosomal dominant hypophosphataemic rickets; ADHR; fibrous dysplasia; X-linked hypophosphataemic rickets; XLH; tumour induced osteomalacia; TIO; hereditary hypophosphataemic rickets with hypercalciuria; HHRH; hypophosphataemic bone disease; HBD; epidermal nevus syndrome; nephrolithiasis; hyperhosphataemic disorder; mild renal insufficiency; tumoural calcinosis; osteoporosis; dermatomyositis; human.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Claim 3; Fig
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    N-PSDB;
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/note= "Fibroblast growth factor
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Best Local Similarity
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  The present invactivities of i calcification,
                                                                                              Polypeptides useful for regulating phosphate transport and calcium metabolism and DNA encoding them for treatment of phosphate and calcium metabolism disorders, including bone formation abnormalities and kidney
                                                            Claim 1;
                                                                                                                                                                                                                                                          11-AUG-2000; 2000JP-0245144.
21-SEP-2000; 2000JP-0287684.
22-DEC-2000; 2000JP-0391077.
19-APR-2001; 2001JP-0121527.
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                                                                                                                                                                                                                                                                                                                                                                                                                      Homo sapiens.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        OST311; phosphoric acid metabolism; calcium metabolism; calcification; vitamin D metabolism; hypophosphataemia; phosphate transport; cytostatic; chromosome 12p13; osteopathic; nephrotropic; antihyperphosphataemic; phosphorus transport; skeletal disorder; bone cancer; osteoporosis;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Human OST311 protein sequence SEQ ID NO:2.
                                                                                                                                                                                                                                                                                                                                                                                                                                                             bone formation abnormality; vitamin D resistance; Paget's disease;
bone calcium deficiency; kidney disorder; kidney function deficiency;
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)B; ABL50577.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                  phosphate leakage; urinary tubule acidosis; Fanconi's
                                                         Page
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t invention describes DNA encoding a polypeptide having the of inhibiting hypophosphataemia, phosphate transport and ion, and regulating vitamin D metabolism in vivo. The
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               100.0%; Score 1360; DB 23; ilarity 100.0%; Pred. No. 7.5e-131; Conservative 0; Mismatches 0;
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RESULT 12
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Best Local (
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   The invention relates to a fibroblast growth factor polypeptide, designated zFGF12, comprising a sequence at least 95 % identical to residues 25 to 251 of the 251 amino acid sequence, given in the specification. The activity of the fibroblast growth factor of the invention may be described as vulnerary. zFGF12 can be used to promote wound healing of the epidermis, to protect and promote recovery of
invention may be described as vulnerary. wound healing of the epidermis, to prote epithelial cells in the gastrointestinal
                                                                                                     healing, protecting and stimul
or radiation, and stimulating
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to other members
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Matches 251
       Human FGF23 protein mutant applicable in gene therapy
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29-MAY-2001;
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RESULT 14
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Best Local Sim
Matches 250;
                              26-DEC-2000;
29-MAY-2001;
                                                                26-DEC-2001;
                                                                                         04-JUL-2002.
                                                                                                                                                 Misc-difference
                                                                                                                                                                                    Synthetic
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          hyperphosphataemia, including gene therapy. The of a FGF23 mutant of the invention.

Note: The present sequence is not shown in the derived from the wildtype human FGF23 sequence the sequence listing (ABB77581).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        The invention relates to a DNA (ABN81575) encoding a protein (ABB77581) FGF23 and mutants FGF23 comprising an amino acid substitution of arginine at position 176 to glutamine and/or position 179 to glutamine or tryptophan. The mutants are generated by introducing the following base changes in the nucleic acid sequence: R1760 mutant is generated by G527A; R179Q is generated by G536A; and R179W is generated by C535T. The protein and encoding DNA are applicable in remedies for hyperphosphataemia, including gene therapy. The present sequence is that
                                                                                                            WO200252009-A1
                                                                                                                                                                                               Homo sapiens
                                                                                                                                                                                                                      mutein.
                                                                                                                                                                                                                                 Human; FGF23;
                                                                                                                                                                                                                                                       Human FGF23
                                                                                                                                                                                                                                                                              28-AUG-2002
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                                                                                                                                                                                                                                                                                                                             ABB77583 standard;
       (CHUS ) CHUGAI SEIYAKU KK
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                                                                                                                                                                                                                                                        mutant R179Q
                              2000JP-0396316.
2001JP-0161370.
                                                                2001WO-JP11482
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                                                                                                                                   "Wildtype Arg
                                                                                                                                                                                                                            hyperphosphataemia; gene therapy; mutant;
                                                                                                                                                                                                                                                                                                                              251
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Pred. No. 1.9e-130;
1; Mismatches 0;
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                                                                                                                                   substituted
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                DB 23;
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                                                                                                                                   γ̈́
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RESULT 15
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Of a FGF23 mutant of the invention in the specification Note: The present sequence is not shown in the specification Note: The present sequence is not shown in the specification Note: The present sequence is sequence given as SEQ I armence listing (ABB77581).
                                             Homo sapiens.
Synthetic.
                                                                                                                                           autosomal dominant hypophosphataemic rickets; ADHR, fibrous dysplasia X-linked hypophosphataemic rickets; XLH; tumour induced osteomalacia; TIO; hereditary hypophosphataemic rickets with hypercalciuria; HHRH; hypophosphataemic bone disease; HBD; epidermal nevus syndrome;
                                                                                                mutein.
                                                                                                                            hypophosphataemic bone disease; HBD nephrolithiasis; hyperphosphataemic
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             The invention relates to a DNA (ABN81575) encoding a protein (ABB77581) FGF23 and mutants FGF23 comprising an amino acid substitution of argining the position 176 to glutamine and/or position 179 to glutamine ord/or position 179 to glutamine ord tryptophan. The mutants are generated by introducing the following base changes in the nucleic acid sequence: R1760 mutant is generated by G527A; R1790 is generated by G536A; and R179W is generated by C535T. Thy protein and encoding DNA are applicable in remedies for hyperphosphataemia, including gene therapy. The present sequence is that
                                                                                                                                                                                                                                               Human fibroblast growth factor-23 (FGF23), R176Q mutant
                                                                                                                                                                                                                                                                                      02-JUL-2002
                                                                                                                                                                                                                Fibroblast growth factor 23;
                                                                                                                                                                                                                                                                                                                                                      AAU79379 standard;
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                                                                                                                 cumoural
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                                                                                                                                                                                                                                                                                                                                                   Protein;
                                                                                                            osteoporosis; dermatomyositis; human; mutant;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       for lowering blood phosphorus level, remedies for hyperphosphatemia -
                                                                                                                                                                                                                                                                                                                                                     251
                                                                                                                                                                                                            FGF23; hypophosphataemic disorder;
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Pred. No. 1.9e-130;
1; Mismatches 0;
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                                                                                                                               disorder; mild
                                                                                                                                                                                            rickets; ADHR; fibrous dysplasia;
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Misc-difference

Location/Qualifiers

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Query Match
Best Local Similarity
Matches 250; Conserv
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            The invention describes an isolated polypeptide (I) comprising a fibroblast growth factor 23 (FGF23) polypeptide or its mutant, variant, homologue or fragment. (I) is useful for treatment of a hypophosphataemic disorder such as autosomal dominant hypophosphataemic rickets (ADHR), x-linked hypophosphataemic rickets (XIH), hereditary hypophosphataemic rickets with hypercalciuria (HHRH), hypophosphataemic bone disease (HBD), epidermal nevus syndrome, fibrous dysplasia tumour induced osteomalacia (TIO), and nephrolithiasis. (I) can also be used in treatment of a hyperphosphataemic disorder such as mild renal insufficiency and tumoural calcinosis. Osteoporosis, conditions (e.g., dermatomyositis) involving deposition of calcium and phosphate in the arteries or soft tissues of
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Sequence
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Novel fibroblast growth factor 23, and polynucleotides encoding the polypeptides, useful for treating hyperphosphataemic disorders such mild renal insufficiency or tumoural calcinosis, or coronary artery
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      WPI; 2002-329399/36
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                                                                                                                                                                                                                                                                                                                                                                                                                       61 VDGAPHQTIYSALMIRSEDAGFVVITGVMSRRYLCMDFRGNIFGSHYFDDENCRFQHQTL 120
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                                                                                                                                                         AEDDSERDPLNVLKPRARMTPAPASCSQELPSAEDNSPMASDPLGVVRGGRVNTHAGGTG 240
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PEGCRPFAKFI 251
                                                               PEGCRPFAKFI
                                                                                                                        AEDDSERDPLNVLKPRARMTPAPASCSQELPSAEDNSPMASDPLGVVRGGRVNTHAGGTG
                                                                                                                                                                                                                                                   ENGYDVYHSPQYHFLVSLGRAKRAFLPGMNPPPYSQPLSRRNEIPLIHFNTPIPRQHTRS
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                251 AA;
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                                                            251
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99.6%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Score 1356; DB 23;
Pred. No. 1.9e-130;
1; Mismatches 0;
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